

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 04:49:48 ; Search time 913 Seconds

(without alignments)
11505.704 Million cell updates/sec

Title: US-09-980-650-6

Perfect score: 2788

Sequence: 1 aaataagcattcttactgctt.....tactagagacataacacg 2788

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:**
1: gb_da:*
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40: em_hugo_mus:*
41: em_hugo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	2788	100.0	2788	6	AX044390 Sequence
2	2659.4	95.4	2692	6	AX044391 Sequence
3	2407.6	86.4	2436	6	AX044392 Sequence
4	2333.2	83.7	2788	6	AX044393 Sequence
5	2204.6	79.1	2692	6	AX044394 Sequence
6	1952.8	70.0	2436	6	AX044395 Sequence
7	1951	70.0	2062	6	AX044385 Sequence
8	1848.2	66.3	7378	6	AR110602 Sequence
9	1848.2	66.3	7378	6	AR151001 Sequence
10	1848.2	66.3	7378	6	AR152424 Sequence
11	1848.2	66.3	7378	6	AR152433 Sequence
12	1848.2	66.3	7378	6	AR184317 Sequence
13	1848.2	66.3	7378	6	AR212558 Sequence
14	1845.4	66.2	1851	6	AR110596 Sequence
15	1845.4	66.2	1851	6	AR150995 Sequence
16	1845.4	66.2	1851	6	AR152418 Sequence
17	1845.4	66.2	1851	6	AR152427 Sequence
18	1845.4	66.2	1851	6	AR184311 Sequence
19	1845.4	66.2	1851	6	AR212552 Sequence
20	1845	66.2	1845	6	E29365 Method for
21	1845	66.2	1845	12	SYNCRVIA
22	1844.8	66.2	3484	6	AR127687 Sequence
23	1844.8	66.2	3484	6	I75356 Sequence 10
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25	1843.4	66.1	1845	6	AR098461 Sequence
26	1843.4	66.1	1845	6	AX441374 Sequence
27	1843.4	66.1	1845	6	AX453870 Sequence
28	1843.4	66.1	1845	6	I41421 Sequence 5
29	1843.4	66.1	3531	6	AR127585 Sequence
30	1843.4	66.1	3531	6	I75254 Sequence 3
31	1507.8	54.1	2062	6	AX044386 Sequence
32	1409.6	50.6	1857	1	BTCRYDE
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38	1220.4	43.8	2815	6	A04445 Synthetic P
39	1220.4	43.8	2815	6	I12419 Sequence 2
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41	1220.4	43.8	3066	6	A04448 Synthetic P
42	1220.4	43.8	3066	6	I12420 Sequence 3
43	1220.4	43.8	3540	1	BTU94191 Bacillus th
44	1220.4	43.8	3550	1	BTCRYIAB
45	1220.4	43.8	3778	1	BACCRSB M3898 B. thuringie

ALIGNMENTS

RESULT 1
AX044390
LOCUS AX044390 2788 bp DNA linear PAT 24-NOV-2000
DEFINITION Sequence 6 from Patent WO0066755.
ACCESSION AX044390
VERSION AX044390.1 GI:11343268
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Christou, P. and Mehlo, L.
TITLES Pesticidal fusions
JOURNAL Patent: WO 0066755-A 6 09-NOV-2000;
Plant Biotechnology Limited (GB)

FEATURES	source	location/Qualifiers
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		/organism="synthetic construct"
		/mol_type="genomic DNA"
		/db_xref="taxon:32630"
		/note="Nucleotide sequence of CRYIa(b)-RTI1 in pFASTBAC1"
BASE COUNT	760 a	684 c 601 g 743 t
ORIGIN		

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Best Local Similarity	100.0%	Pred. No. 0		
Matches 2788; Conservative	0	Mismatches	0	Gaps 0

OY	1	AAATAGATTTTAACTGTTTTCGAAACGTTTGTAAATAAAAAACCTATAAATATTCGG	60
Db	1	AAATAGATTTTAACTGTTTTCGTAACGTTTGTATAAAAAACCTATAAATATTCGG	60
OY	61	GATTATTCATACCGTCCCAACCATCGGGCGCGGATCCATGAGCAACAACCCAAACATCAAC	120
Db	61	GATTATTCATACCGTCCCAACCATCGGGGCGGATCCATGAGCAACAACCCAAACATCAAC	120
OY	121	GAATGCATTTCCATACACTGCTTGAAGTAACCCAGAAATTGAAGTACTTGTGTGAGAACCC	180
Db	121	GAATGCATTTCCATACACTGCTTGAAGTAACCCAGAAATTGAAGTACTTGTGTGAGAACCC	180
OY	181	ATTGAAACCCGGTATCACTCCCATCGACATCTCCTTGTCCCTTACACAGTTTCTGCCTCAGC	240
Db	181	ATTGAAACCCGGTATCACTCCCATCGACATCTCCTTGTCCCTTACACAGTTTCTGCCTCAGC	240
OY	241	GAGTTTCGTCCAGGTCCTGGGTTGCTTCTCGGACTAAGTTGACATCATCTGGGGTATCTTT	300
Db	241	GAGTTTCGTCCAGGTCCTGGGTTGCTTCTCGGACTAAGTTGACATCATCTGGGGTATCTTT	300
OY	301	GSTCCATCTCAATGGGAGTGCATTTCCGTGGCAAAATTGACAGTGTATCAACCAAGAGATC	360
Db	301	GSTCCATCTCAATGGGAGTGCATTTCCGTGGCAAAATTGACAGTGTATCAACCAAGAGATC	360
OY	361	GAAGAGTTTCGCCAGGAACCCAGGCCATCTCTAGTTTGAAGATTGACAACTCTTACCAA	420
Db	361	GAAGAGTTTCGCCAGGAACCCAGGCCATCTCTAGTTTGAAGATTGACAACTCTTACCAA	420
OY	421	ATCTATGCAGAGAGCTTTCAGAGAGTGGGAAGCCGATCTTACTTAAACCAGCTCTCCGCGAG	480
Db	421	ATCTATGCAGAGAGCTTTCAGAGAGTGGGAAGCCGATCTTACTTAAACCAGCTCTCCGCGAG	480
OY	481	GAATATGCGTATTCATTTCAAGACATGAACACGCGCTTGACCAACAGCTATCCCATTTGTC	540
Db	481	GAATATGCGTATTCATTTCAAGACATGAACACGCGCTTGACCAACAGCTATCCCATTTGTC	540
OY	541	GCAGTTCAGAACTACCAAGTTCCTCTCTTGTCCGTACGTTTCAGACAGCTAATCTTTCAC	600
Db	541	GCAGTTCAGAACTACCAAGTTCCTCTCTTGTCCGTACGTTTCAGACAGCTAATCTTTCAC	600
OY	601	CTCAGCGGCTTCGAGACGTTTACGCGTGTGGGCAAAAGTGGGGGATTCGATGTGCAAC	660
Db	601	CTCAGCGGCTTCGAGACGTTTACGCGTGTGGGCAAAAGTGGGGGATTCGATGTGCAAC	660
OY	661	ATCAATAGCCGTTTACACAGACCTTACTAGCTGATTGGAACTTACACCGACACGCTGTT	720
Db	661	ATCAATAGCCGTTTACACAGACCTTACTAGCTGATTGGAACTTACACCGACACGCTGTT	720
OY	721	CGTTGGTACAAACCTGCGCTTGGAGCGTGTCTGGGGTCTTGATTTCTTGAAGATTGGATTAA	780
Db	721	CGTTGGTACAAACCTGCGCTTGGAGCGTGTCTGGGGTCTTGATTTCTTGAAGATTGGATTAA	780
OY	781	TACAACCAAGTTCAGAGAGAAATTGACCTTCACAGTTTGGACATTGTGCTCTCTCCCG	840
Db	781	TACAACCAAGTTCAGAGAGAAATTGACCTTCACAGTTTGGACATTGTGCTCTCTCCCG	840
OY	841	AACTATGACTCAGAACTTACCCTTATCGGTACAGTGTCCCAACTTCCAGAGAAATCTAT	900
Db	841	AACTATGACTCAGAACTTACCCTTATCGGTACAGTGTCCCAACTTCCAGAGAAATCTAT	900

QY	901	CTTAAACCAGTTCCTTGGAACTTCGACGGTACGTCCTCGTGGTTCTGCCCAAGCTATCGAA	960
Dp	901	ACTAACCCAGTTCCTTGGAACTTCGACGGTACGTCCTCGTGGTTCTGCCCAAGCTATCGAA	960
QY	961	GGCTCCATTCAGGAGCCCACTTGATGAGCATCTTGGAAAGCATTAAGCATTAATCTACACCGAT	1020
Dp	961	GGCTCCATTCAGGAGCCCACTTGATGAGCATCTTGGAAAGCATTAATCTACACCGAT	1020
QY	1021	GCTCAACAGAGAGGATTTACTGGTCTGGACACCAAGATCATGGCTCTCCAGTTGAGATT	1080
Dp	1021	GCTCAACAGAGAGGATTTACTGGTCTGGACACCAAGATCATGGCTCTCCAGTTGAGATT	1080
QY	1081	AGCGGAGCCGAGTTTACCTTCCCTCTAATGGAACATAAGGAAAGCGCGCTCCAAACAA	1140
Dp	1081	AGCGGAGCCGAGTTTACCTTCCCTCTAATGGAACATAAGGAAAGCGCGCTCCAAACAA	1140
QY	1141	CGTATCGTGTCTCAACTAGGTCAGAGGTGTCTACGAACCTTGTCTTCCACTTGTACAGA	1200
Dp	1141	CGTATCGTGTCTCAACTAGGTCAGAGGTGTCTACGAACCTTGTCTTCCACTTGTACAGA	1200
QY	1201	AGACCCCTTCAATACGGATTCGAACACAGCAACTTTCGGTCTTGGACGGAAAGAGTTC	1260
Dp	1201	AGACCCCTTCAATACGGATTCGAACACAGCAACTTTCGGTCTTGGACGGAAAGAGTTC	1260
QY	1261	GCCCTATGGAACTCTTCTTAACCTTGCACATCCGCTTTTACAGAAAGAGGGAACCGTTGAT	1320
Dp	1261	GCCCTATGGAACTCTTCTTAACCTTGCACATCCGCTTTTACAGAAAGAGGGAACCGTTGAT	1320
QY	1321	TCCTTTGGACGAATATCCCAACAGAACACAAATGTGCCACCCAGGCAAGATTTCTCCAC	1380
Dp	1321	TCCTTTGGACGAATATCCCAACAGAACACAAATGTGCCACCCAGGCAAGATTTCTCCAC	1380
QY	1381	AGTTTGAGCCACGTGTCCATGTTCCGTTCCGGATTACAGCAACAGTTCGGTAGCATATC	1440
Dp	1381	AGTTTGAGCCACGTGTCCATGTTCCGTTCCGGATTACAGCAACAGTTCGGTAGCATATC	1440
QY	1441	AGAGCTCCTATGTTCTCATGGATTCATCGTAGTGTGAGTTCAACAATATCATTTCTTCC	1500
Dp	1441	AGAGCTCCTATGTTCTCATGGATTCATCGTAGTGTGAGTTCAACAATATCATTTCTTCC	1500
QY	1501	TCTCAATATCACCCAAATCCCAATGACAGCTATCAACTTGGATCTGGAACCTTCTGTG	1560
Dp	1501	TCTCAATATCACCCAAATCCCAATGACAGCTATCAACTTGGATCTGGAACCTTCTGTG	1560
QY	1561	GTGAAGGAGCAGGAGCTTCAACAGAGGTGATTTCTTAGAAGAACTCTTCTCGGCGAGATT	1620
Dp	1561	GTGAAGGAGCAGGAGCTTCAACAGAGGTGATTTCTTAGAAGAACTCTTCTCGGCGAGATT	1620
QY	1621	AGCACCTCTCAGAGTTAACAATACCTGCACCACTTTCTCAAAGATATCGGTACAGATTGCT	1680
Dp	1621	AGCACCTCTCAGAGTTAACAATACCTGCACCACTTTCTCAAAGATATCGGTACAGATTGCT	1680
QY	1681	TACCATCTACCACTTAATCTTGCAATTCACAACCTTCACATCGACGGAAGGCTATCAATCAG	1740
Dp	1681	TACCATCTACCACTTAATCTTGCAATTCACAACCTTCACATCGACGGAAGGCTATCAATCAG	1740
QY	1741	GGTAACTTCTCCGAAACCATGTCAAGCGGACGCAACTTGCATATCCGACGCTTCAAGAAC	1800
Dp	1741	GGTAACTTCTCCGAAACCATGTCAAGCGGACGCAACTTGCATATCCGACGCTTCAAGAAC	1800
QY	1801	GTCGGTTTCACTACTCCCTTTCAACTTCCTTAAGGGATCAAGCGTTTCAACGCTTAAGCGCT	1860
Dp	1801	GTCGGTTTCACTACTCCCTTTCAACTTCCTTAAGGGATCAAGCGTTTCAACGCTTAAGCGCT	1860
QY	1861	CATGTGTTCAATTTCTGGCAATGAAGTGAATTGAACCGTATTTGAGTTTGTCTCGCGAA	1920
Dp	1861	CATGTGTTCAATTTCTGGCAATGAAGTGAATTGAACCGTATTTGAGTTTGTCTCGCGAA	1920
QY	1921	GTAACTTTCGAGGCTGAGTACTCGAAGATTCATGCTGAAGTTTGTATGGAATCCTTAGGCCA	1980
Dp	1921	GTAACTTTCGAGGCTGAGTACTCGAAGATTCATGCTGAAGTTTGTATGGAATCCTTAGGCCA	1980
QY	1981	TATGTCGATATGTAAGTTCGAATATGATATGTTAGTTAGGATGGAAGATTCACA	2040

Db	1981	TAGTGGCTATCTGTAAGCTCGAAATGCTCTATGTGTGATGTTAGGAGTGGAAAGATTCCACA	2040
Qy	2041	ACGGAAACGCATATACAGTTGTGGCCATGCAAGTCTAAATACAGATGCAATACAGTCTTGGAA	2100
Db	2041	ACGGAAACGCATATACAGTTGTGGCCATGCAAGTCTAAATACAGATGCAATACAGTCTTGGAA	2100
Qy	2101	CTTTGAAAAGGACATATCTATTTGGATCTTAATGGAAAGTGTTTAACTTACTTAACGGGTACA	2160
Db	2101	CTTTGAAAAGGACATATCTATTTGGATCTTAATGGAAAGTGTTTAACTTACTTAACGGGTACA	2160
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Db	2161	GTCCGGAGTCTATGTGATGATCTATGATTTGCCAATACCTGCTCAACTGATGCCACCGCT	2220
Qy	2221	GGCAAAATATGGGATTAATGGAAACCATTCATTAATCCCAAGTCTATAGTCTAGTTTACAGCGA	2280
Db	2221	GGCAAAATATGGGATTAATGGAAACCATTCATTAATCCCAAGTCTATAGTCTAGTTTACAGCGA	2280
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Qy	2401	TGTGCTTGCAAGCAAAATATGAGACAAAGTATGAGATGAGACATGATGCAAGTAAAGGCTG	2460
Db	2401	TGTGCTTGCAAGCAAAATATGAGACAAAGTATGAGATGAGACATGATGCAAGTAAAGGCTG	2460
Qy	2461	AACAAACAGTGGGCTCTTTATGACAGATGGTTCATTAACGTCCTCAGCAAAACCGAATATTT	2520
Db	2461	AACAAACAGTGGGCTCTTTATGACAGATGGTTCATTAACGTCCTCAGCAAAACCGAATATTT	2520
Qy	2521	GCCTTACAAGATTTCTTAATATACGGGAAACAGTTTGAATCTCTCTTGTGGCCTG	2580
Db	2521	GCCTTACAAGATTTCTTAATATACGGGAAACAGTTTGAATCTCTCTTGTGTGGCCTG	2580
Qy	2581	CATCCTCTGGCCCAACAGATGATGTTTCAAGAATGATGAAACCATTTTAAATTTGTATAGTG	2640
Db	2581	CATCCTCTGGCCCAACAGATGATGTTTCAAGAATGATGAAACCATTTTAAATTTGTATAGTG	2640
Qy	2641	GATTGGTGTAGATGTGTAGAGCGGATCGATCCGAGCCTTTAAACAAATCATTTCTTAACTCTC	2700
Db	2641	GATTGGTGTGTAGATGTGTAGAGCGGATCGATCCGAGCCTTTAAACAAATCATTTCTTAACTCTC	2700
Qy	2701	TCCATGGTGACCCCAACCAAAATATGCTTACCATTAATTTTGTATAGACATTAACAAGCTTG	2760
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Db	2761	TCGAGAAGTACTAGAGATCATTAATCAG	2788
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LOCUS	AX044391	2692 bp	DNA linear PAT 24-NOV-2000
DEFINITION	Sequence 7 from Patent WO006755.		
ACCESSION	AX044391		
VERSION	AX044391.1	GI:11343269	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS	Christou, P. and Menlo, L.		
TITLE	Peptidic fusions		
JOURNAL	Patent: WO 006755-A 7 09-NOV-2000;		
FEATURES	Plant Bioscience Limited (GB)		
SOURCE	Location/Qualifiers		
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[illegible]

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Db 1081 AGCGGGCCCGAGTTAACTTCTCTCTATGGAATATGGAAGAGCGCGCTCCACAA 1140

Qy 1141 CGTATCGTGTCTCAACTAGTCAAGGAGTCTACAGAACCTTGCTTCCACCTTGATGAGA 1200

Db 1141 CGTATCGTGTCTCAACTAGTCAAGGAGTCTACAGAACCTTGCTTCCACCTTGATGAGA 1200

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Qy 1861 CATGTGTTCAATTTCTGCAATGAGTATGATGATGATGATGATGATGATGATGATGATG 1920

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Qy 1981 TATGTGCTATCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040

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Qy 2041 ACGGAAGCGAATACAGTTGTGGCATGCAAGTCTAATACAGATGCAATACAGTCTTGA 2100

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Qy 2221 GGCATAATATGAGATGAGAACCATCATATATCCAGATCTAGTCTATGATGATGATG 2280

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Qy 2281 CATCAGGAGACAGTGTATGACACACTTACGGTCAACCAATTTATGCGTTATGATG 2340

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Db 2581 CATCTCTGCGCAACAGATGATGATGATGATGATGATGATGATGATGATGATGATG 2640

Qy 2641 GATTGCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2661

Db 2641 GATTGCTGTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2661

RESULT 3

AX044392 2436 bp DNA linear PAT 24-NOV-2000

LOCUS AX044392 Sequence 8 from Patent WO0066755.

DEFINITION AX044392

ACCESSION AX044392.1 GI:11343270

VERSION AX044392.1

KEYWORDS

SOURCE

ORGANISM

synthetic construct

synthetic construct

artificial sequences.

REFERENCE

1

AUTHORS Christou, P. and Menlo, L.

TITLE Pesticidal fusions

JOURNAL Patent: WO 0066755-A 8 09-NOV-2000;

Plant Bioscience Limited (GB)

FEATURES

source

1. 2436

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="nucleotide sequence of CryIa(b)-RmB3 in pFASTBAC1"

BASE COUNT 654 a 617 c 521 g 644 t

ORIGIN

Query Match 86.4%; Score 2407.6; DB 6; Length 2436;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2416; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy	1	AAATAAGTATTTTACCTGTTTTTCGTAACAAGTTTGTGATAAATAAAAAACCTATAAATATATTC	60
Db	1	AAATAAGTATTTTACCTGTTTTTCGTAACAAGTTTGTGATAAATAAAAAACCTATAAATATATTC	60
Qy	61	GATTATTCATACCGTCCCAACCATCGGGCGGGATCCATGAGCAACAACCCAAACATCAAC	120
Db	61	GATTATTCATACCGTCCCAACCATCGGGCGGGATCCATGAGCAACAACCCAAACATCAAC	120
Qy	121	GAATGCATTTCATACCACTGCTTGAGTAACCCAGAGTTGAAGTACTTGGTGGAGAACGC	180
Db	121	GAATGCATTTCATACCACTGCTTGAGTAACCCAGAGTTGAAGTACTTGGTGGAGAACGC	180
Qy	181	ATTGAAACCGGGTACATCCCATCGACATCTCCCTGCTCTTGACACAGTTTCTGCTCAGC	240
Db	181	ATTGAAACCGGGTACATCCCATCGACATCTCCCTGCTCTTGACACAGTTTCTGCTCAGC	240
Qy	241	GAGTTGCTGCCAGGTGCTGGGTTGGTTCTCGGACTAGATTGACATCATCTGGGGTATCTTT	300
Db	241	GAGTTGCTGCCAGGTGCTGGGTTGGTTCTCGGACTAGATTGACATCATCTGGGGTATCTTT	300
Qy	301	GGTCCATCTCAATGGGATGCATCTCTGCTGTGAATTAGACAGTTGATCAACAGAGATC	360
Db	301	GGTCCATCTCAATGGGATGCATCTCTGCTGTGAATTAGACAGTTGATCAACAGAGATC	360
Qy	361	GAAAGATTCCGCCAGAACCAAGGCCATCTCTAGTTGGAAAGGATGAGCAATCTCTACAA	420
Db	361	GAAAGATTCCGCCAGAACCAAGGCCATCTCTAGTTGGAAAGGATGAGCAATCTCTACAA	420
Qy	421	ATCTATGACAGAGCTTCAAGAGTGGAGACCGCATCTTAACCAACGCTCTCCGGAG	480
Db	421	ATCTATGACAGAGCTTCAAGAGTGGAGACCGCATCTTAACCAACGCTCTCCGGAG	480
Qy	481	GAAATGGGATTAATTAATCAAGATGAAGAACGGCCCTTGACCAAGCATTCCTCATTCCTC	540
Db	481	GAAATGGGATTAATTAATCAAGATGAAGAACGGCCCTTGACCAAGCATTCCTCATTCCTC	540
Qy	541	GCAGTCCAGAACTACCAAGTTCCTCTCTGTCGGTGTACGTTCAAGCAGCTAATCTTCAC	600
Db	541	GCAGTCCAGAACTACCAAGTTCCTCTCTGTCGGTGTACGTTCAAGCAGCTAATCTTCAC	600
Qy	601	CTCAGCGCTTTCAGAGAGTTAGCGTGTTTGGGCAAAAGTGGGGATTCGATGCTGCACAC	660
Db	601	CTCAGCGCTTTCAGAGAGTTAGCGTGTTTGGGCAAAAGTGGGGATTCGATGCTGCACAC	660
Qy	661	ATCAATAGCCGTTCACAGACCTTAAGCTTAAGTGGAAACTACACGACCAACGCTGTT	720
Db	661	ATCAATAGCCGTTCACAGACCTTAAGCTTAAGTGGAAACTACACGACCAACGCTGTT	720
Qy	721	CGTTGGTACAAACACTGGGCTTGGAGCGTGTCTGGGGCTCTGAATTCAGAGATTGGATTAGA	780
Db	721	CGTTGGTACAAACACTGGGCTTGGAGCGTGTCTGGGGCTCTGAATTCAGAGATTGGATTAGA	780
Qy	781	TACAAACCAAGTTCAGAGAGAAATTGACCTTCAAGTTTGGACATTGGTCTCTCTCCG	840
Db	781	TACAAACCAAGTTCAGAGAGAAATTGACCTTCAAGTTTGGACATTGGTCTCTCTCCG	840
Qy	841	AACATAGCTCCAGAACCTTACCCTTACCGTAAGTGTCCCACTTACCCAGAGAAATCTAT	900
Db	841	AACATAGCTCCAGAACCTTACCCTTACCGTAAGTGTCCCACTTACCCAGAGAAATCTAT	900
Qy	901	ACTAACCCAGTTCTTGAGAACTTGACGCGTACGTTCCGTGGTCTTGCCCAAGGTATGGA	960
Db	901	ACTAACCCAGTTCTTGAGAACTTGACGCGTACGTTCCGTGGTCTTGCCCAAGGTATGGA	960
Qy	961	GGCTCCATCAGAGAGCCCAACTTGATGACACTTTGAAACAGCATTAATCAACCGAT	1020
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Qy	1021	GCTCACAGAGAGAGTATTACTGCTTGGAACACAGATCATGGCTCTTCCAGTTGGATTTC	1080
Db	1021	GCTCACAGAGAGAGTATTACTGCTTGGAACACAGATCATGGCTCTTCCAGTTGGATTTC	1080

QY	1081	AGGGGGCCCGAGTTTACCTTTTCTCTCTATATGGAATCTATGGGAAAGCCGCTCCACAACAA	1140
Db	1081	AGGGGGCCCGAGTTTACCTTTTCTCTCTATATGGAATCTATGGGAAAGCCGCTCCACAACAA	1140
QY	1141	CGATGCTGTCAATCTAGTCAAGGGGTGTCTACAGAACCTTGTCTTCCACTTGTACAGA	1200
Db	1141	CGATGCTGTCTCAACTTAGGTCAAGGGGTGTCTACAGAACCTTGTCTTCCACTTGTACAGA	1200
QY	1201	AGACCCCTTCATATCCGATTCACAACAACGACAACCTTCCGTTCTTGAAGGAAACAGATTTC	1260
Db	1201	AGACCCCTTCATATCGGTATTCACAACAACGACAACCTTCCGTTCTTGAAGGAAACAGATTTC	1260
QY	1261	GCCCTATGGAACCTCTTCTTCACTTGGCATTCGCTGTTTACAGAAAGCGGAAACCGTTGAT	1320
Db	1261	GCCCTATGGAACCTCTTCTTCACTTGGCATTCGCTGTTTACAGAAAGCGGAAACCGTTGAT	1320
QY	1321	TTCCTGGAAGGAATTCACACAGAAACAACATATGCCACCGAGGACAGAAATTCTCCAC	1380
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QY	1381	AGGTTGAGCCACGTCGTCAATGTTCCGTTCCGATTCAAGCAACAGTTCCGTGAGCATATC	1440
Db	1381	AGGTTGAGCCACGTCGTCAATGTTCCGTTCCGATTCAAGCAACAGTTCCGTGAGCATATC	1440
QY	1441	AGAGCTCTATGTTCTCATGAGTTCATCGTAGTGTGAGTTCAACATATCATCTTCTCC	1500
Db	1441	AGAGCTCTATGTTCTCATGAGTTCATCGTAGTGTGAGTTCAACATATCATCTTCTCC	1500
QY	1501	TCTCAATATCACCCCAATTCCTCATTTGACCAAGTCTACTAACCTTGGATCTGGAACTTCTGTC	1560
Db	1501	TCTCAATATCACCCCAATTCCTCATTTGACCAAGTCTACTAACCTTGGATCTGGAACTTCTGTC	1560
QY	1561	GTEGAAGAAGCAGAGCTTTCACAGAGGTGATATTTCTTAGAAGAACCTTCTCTGGCAGATT	1620
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QY	1681	TAGGCATCTACCACTAATTGCAATTCACACCTTCATGACAGGAAGGCTTATCAATTAG	1740
Db	1681	TAGGCATCTACCACTAATTGCAATTCACACCTTCATGACAGGAAGGCTTATCAATTAG	1740
QY	1741	GGTAACTTCCCGGCAACCATGTCAAGCGGACGAACTTGCATCCGGGAGCTTCAAGAAC	1800
Db	1741	GGTAACTTCTCCGGCAACCATGTCAAGCGGACGAACTTGCATCCGGGAGCTTCAAGAAC	1800
QY	1801	GTCGGTTTCACTACTCTTTTCAACTTCTCTAAACGATCAAGGCTTTTCAACCTTACGCT	1860
Db	1801	GTCGGTTTCACTACTCTTTTCAACTTCTCTAAACGATCAAGGCTTTTCAACCTTACGCT	1860
QY	1861	CATGTGTTCAATCTGGCAATGAAGTGTACATTGACCGTATGAGTTGTGTGCTTGGCA	1920
Db	1861	CATGTGTTCAATCTGGCAATGAAGTGTACATTGACCGTATGAGTTGTGTGCTTGGCA	1920
QY	1921	GTTACCTTTCGAGGCTGAGTCTAGAAATCATGCGATGTTTGTATGATCCTGAGCCCA	1980
Db	1921	GTTACCTTTCGAGGCTGAGTCTAGAAATCATGCGATGTTTGTATGATCCTGAGCCCA	1980
QY	1981	TAGTGCCTATCGTAGGTGCAATATGATCTATATGTTGATGTTAGGATGGAAGATTCCACA	2040
Db	1981	TAGTGCCTATCGTAGGTGCAATATGATCTATATGTTGATGTTAGGATGGAAGATTCCACA	2040
QY	2041	ACGGAAGCGCAATACAGTTGTGGCCATGCAAGTCTTAATCAGATGCAATATCAGCTCTGGA	2100
Db	2041	ACGGAAGCGCAATACAGTTGTGGCCATGCAAGTCTTAATCAGATGCAATATCAGCTCTGGA	2100
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Db	2101	CTTTGAAAGAGCAATACTATTCGATCTTAATGGAAGGTTTAACTTACCGGTTACA	2160
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Db	2161	GTCCGGGAGCTTAATGTATGATCTTAATGATTGCAATACCTGCTGCAACTGATGCCACCGCT	2220
Qy	2221	GGCAAAATATGGATTAATGGAACCAATCATMAATCCCAAGTCTAGTCTAGTTTAAAGCGA	2280
Db	2221	GGCAAAATATGGATTAATGGAACCAATCATMAATCCCAAGTCTAGTCTAGTTTAAAGCGA	2280
Qy	2281	CATCAGGGAACAGTGTGTACCACTTACGCTGCAAAACCAACTTATATGCCGTAGTCAAG	2340
Db	2281	CATCAGGGAACAGTGTGTACCACTTACGCTGCAAAACCAACTTATATGCCGTAGTCAAG	2340
Qy	2341	GTGGGCTTCCACTAATTAATACACAACTTTTGTATGCAACCAATGTTGGGCTATATGCTC	2400
Db	2341	GTGGGCTTCCACTAATTAATTAACAAACCTTTTGTATGCAACCAATGTTGGGCTATATGCTC	2400
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ACCESSION	AX044393		
VERSION	AX044393.1	GI:11343271	
KEYWORDS			
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ORGANISM			
REFERENCE	1	synthetic construct	
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TITLE	Peucedal fusions	artificial sequences.	
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ORIGIN			
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Best Local Similarity	90.7%; Pred. No. 0;		
Matches 2534; Conservative	0; Mismatches 248; Indels 12; Gaps 4		
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Db	1	AAATAAGTATTTTACTGTTTTCGTAAACAGTTTGTATATAAAAAACCATAAATATTCGG	60
Qy	61	GATTATTCATACCGTCCCAACCATCGGGGCGGATTCATGAGCAACCAACCAACATCAAC	120
Db	61	GATTATTCATACCGTCCCAACCATCGGGGCGGATTCATGAGCAACCAACCAACATCAAC	120
Qy	121	GAATGATTTCCATATCAACTGCTGTGAGTAAACGAGAAGTTGAAGTACTTGGTGGAGACGC	180
Db	121	GAATGATTTCCATATCAACTGCTGTGAGTAAACGAGAAGTTGAAGTACTTGGTGGAGACGC	180
Qy	181	ATTGAAACCGGTTTACATCTCCATCGACATCTCTCTGTCTTGAACAACAGTTTCTGCTCAGC	240
Db	181	ATTGAAACCGGTTTACATCTCCATCGACATCTCTCTGTCTTGAACAACAGTTTCTGCTCAGC	240
Qy	241	GAGTTCGTCGACAGGTCGCTGGGTTGCTTCGGAAGTATGATGATCATCTGGGGTATCTTT	300
Db	241	GAGTTCGTCGACAGGTCGCTGGGTTGCTTCGGAAGTATGATGATCATCTGGGGTATCTTT	300
Qy	301	GGTCCATCTCAATGGGATGATCTTCGCTGTCGAAATTTGACAGTTGATCAACAGAGATC	360
Db	301	GGTCCATCTCAATGGGATGATCTTCGCTGTCGAAATTTGACAGTTGATCAACAGAGATC	360
Qy	361	GAAAGATTTCGCAAGAACGAGGCATCTTAGGTGGAAAGATTGACAAATCTTAACAA	420

Dp	361	GAAGAGTTCCGCCAGGAACGAGCCATCTCTAAGTTGGAAAGATTGAGCAATCTCTACCA	420
Qy	421	ATCTATGCAAGAGCTTCAGAGATGGGAAGCCGATCTTAACCAACGCTCTCCGAG	480
Dp	421	ATCTATGCAAGAGCTTCAGAGATGGGAAGCCGATCTCTAACCAACGCTCTCCGAG	480
Qy	481	GAATGGGTAATTCAAATTCACGACATGAAACAGGCGCTTGACCAAGATATCCCATTTGTC	540
Dp	481	GAATGGGTAATTCAAATTCACGACATGAAACAGGCGCTTGACCAAGATATCCCATTTGTC	540
Qy	541	GCAGTCCAGAACTACCAAGTTCCCTCTTGTCCGTGACCTTAAGCAGCTAAATCTTCAC	600
Dp	541	GCAGTCCAGAACTACCAAGTTCCCTCTTGTCCGTGACCTTAAGCAGCTAAATCTTCAC	600
Qy	601	CTCAGCGTGCCTTGAGACGTTAAGCTGTTTGGCAAGGTGGGGATTGATGCTGCACCC	660
Dp	601	CTCAGCGTGCCTTGAGACGTTAAGCTGTTTGGCAAGGTGGGGATTGATGCTGCACCC	660
Qy	661	ATCATATGCCGTTTACCAACGACCTTAAGCTGATTTGGAAACTACACCCGACACGCTGTT	720
Dp	661	ATCATATGCCGTTTACCAACGACCTTAAGCTGATTTGGAAACTACACCCGACACGCTGTT	720
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Dp	721	CGTTGGTAACAACATGGCTTTGAGCGGTCTGGGGGTCTGATTTCTAGATTTGAGATTAGA	780
Qy	781	TACAACGAGTTACAGAGAGAAATTGACCCCTCAGACTTTGGACAATTTGTTCTCTTCCTCCG	840
Dp	781	TACAACGAGTTACAGAGAGAAATTGACCCCTCAGACTTTGGACAATTTGTTCTCTTCCTCCG	840
Qy	841	AACATATGATCTTCAGAACCTTACCTTATCCGTAACAGTGTCCCACTTACCAAGAAATCTAT	900
Dp	841	AACATATGATCTTCAGAACCTTACCTTATCCGTAACAGTGTCCCACTTACCAAGAAATCTAT	900
Qy	901	ACTAATCCAGTCTTGGAACTTCGAGAGTTCGCGTGGTTCTGGCCAAAGATATGAA	960
Dp	901	ACTAATCCAGTCTTGGAACTTCGAGAGTTCGCGTGGTTCTGGCCAAAGATATGAA	960
Qy	961	GGCTCCATCAAGAGACCCCACTTGATGGAACATCTTGAACAGCATATATCTACACCGAT	1020
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Dp	1021	GCTCAACAGAGAGATTAATTAAGTCTTGACACACGATCATGCGCTCTCCAGTTGATTC	1080
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Qy	1141	CGTATCGTGTCTCAACTAGAGTCAAGGAGTGTACAGAACTTGTCTTCACCTTGTAAGA	1200
Dp	1141	CGTATCGTGTCTCAACTAGAGTCAAGGAGTGTACAGAACTTGTCTTCACCTTGTAAGA	1200
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Dp	1261	GCCTATGGAACCTCTTCTTAATCTTCCATCCGCTCTTTACAGAAAGAGGGCAACGGTTGAT	1320
Qy	1321	TCCTTGGACGAATCCCAACAGAACAAATATGTCACCCAGGCAAGATTTCTCCAC	1380
Dp	1321	TCCTTGGACGAATCCCAACAGAACAAATATGTCACCCAGGCAAGATTTCTCCAC	1380
Qy	1381	AGGTTGAGCCACGTTGCTCATTTGCTCGTTCCGGATTACAGCAACAGTTCCGTGAGATCATC	1440
Dp	1381	AGGTTGAGCCACGTTGCTCATTTGCTCGTTCCGGATTACAGCAACAGTTCCGTGAGATCATC	1440
Qy	1441	AGAGTCCCTATGTTCTCATGGATTCATCGTATGAGTCTAGTTCAACAATATGATTCCTTCC	1500
Dp	1441	AGAGTCCCTATGTTCTCATGGATTCATCGTATGAGTCTAGTTCAACAATATGATTCCTTCC	1500

Db	1441	AGAGCTCTATGTTCTCTTGGATACACCGTAGTGTGATGTCACACAACTATCGATCC	1500
Qy	1501	TCTCAAAATACCCCAAAATCCCAATGACCAAGTCTACTAACTTTGGATCTGCAATTTCTGTC	1560
Db	1501	GATAGTATTACTCAAAATCCCTGCAGTGAAG---GAAAATTTCTCTTCAACGGTGTCTGTC	1557
Qy	1561	GTGAAGGACCAAGCTTTCACAGAGGTGATATTCTTAGAAGAACCTTCTCCCTGGCCACATT	1620
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Qy	1915	GCCGGAATTACCTTCGAGGCTGAGTACTGAGAAATTCATGCTGATGTTTGTATGATTCCTG	1974
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Qy	2335	GTCGAAGGTGGCTTCTCTACTAATATATACAAACTTTTGTATCAACCATTTGTTGGGCTAT	2394
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ACCESSION	AX044394		
VERSION	AX044394.1	GI:11343272	
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ORGANISM	synthetic construct		
REFERENCE	1		
AUTHORS	Christou, P. and Menlo, L.		
TITLE	Pesticial fusions		
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Best Local Similarity	90.2%; Pred. No. 0;		
Matches 2406; Conservative	0; Mismatches 249; Indels 12; Gaps 4;		
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Db	1	AAATAGATTATTTACTGTTTTCGTACAGTTTGTATATAAAAAACCCTATATAATTTCCG	60
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Db	61	GATTATTCATACCGGCCACCATATGGGGCGGATCCATGACCAACCCAAACATCAAC	120
Oy	121	GAATGATTCATATCAACATCTGTTGAGTAAACCAGAAAGTTGAAGTACTTGTGTGAAACGC	180
Db	121	GAATGATTCATATCAACATCTGTTGAGTAAACCAGAAAGTTGAAGTACTTGTGTGAAACGC	180
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Oy	241	GAGTTGTCGACAGGCTGGGTTCTTCGAGATGTTGACATCATCTGGGGTATCTTT	300
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Oy	301	GGTTCATCTCAATGGGATGATTCCTGCTGCAATGGAAGAGTTGATCAACCAAGAGATC	360
Db	301	GGTTCATCTCAATGGGATGATTCCTGCTGCAATGGAAGAGTTGATCAACCAAGAGATC	360
Oy	361	GAAAGTTGCGCAGAAACAGGCCATCTCTAGTTGGAAAGATTTGAGCAATCTTCAACAA	420
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Db 2635 ATAGTGATGTGTAGATGAGGC 2661

RESULT 6

AX044395 2436 bp DNA linear PAT 24-NOV-2000

LOCUS Sequence 11 from Patent W0006755.

DEFINITION AX044395

ACCESSION AX044395

VERSION AX044395.1 GI:11343273

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

REFERENCE 1

AUTHORS Christou, P. and Mehlo, L.

TITLE Pesticidal fusions

JOURNAL Patent: WO 006755-A 11 09-NOV-2000;

Plant Bioscience Limited (GB)

FEATURES

Source 1..2436

Location/Qualifiers

/organism="synthetic construct"

/mol_type="genomic DNA"

/db_xref="taxon:32630"

/note="Nucleotide sequence of CtryIA(c)-RTB3 in pFASTBAC1"

BASE COUNT 660 a 597 c 527 g 652 t

ORIGIN

Query March 70.0%; Score 1952.8; DB 6; Length 2436;

Best Local Similarity 88.8%; Pred. No. 0;

Matches 2162; Conservative 0; Mismatches 262; Indels 12; Gaps 4;

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Db 1 AAATAAGTATTTTACTGTTTCTGTAACAGTTTGTATATAAAAACTATATAATTTCCG 60

Qy 61 GATTATTCATACCGTCCCAACCATCGGGCGCGGATCATGAGAACAAACCAACATTCAC 120

Db 61 GATTATTCATACCGTCCCAACCATCGGGCGCGGATCATGAGAACAAACCAACATTCAC 120

Qy 121 GAATGATTCATACCACTGCTTGAAGTAACCCAGAAAGTTGAAGTACTTGGTGAAGACG 180

Db 121 GAATGATTCATACCACTGCTTGAAGTAACCCAGAAAGTTGAAGTACTTGGTGAAGACG 180

Qy 181 ATTGAACCGGTTAAGCTCCATGACATCTCTTGTCTTGACACAGTTTCTGCTCAGC 240

Db 181 ATTGAACCGGTTAAGCTCCATGACATCTCTTGTCTTGACACAGTTTCTGCTCAGC 240

Qy 241 GAGTTCGCGGCGAGGCTGGGTTGCTTCCGGAAGTGAAGTGAATCATCTGGGATTTCTT 300

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Qy 301 GGTTCATCTCAATGGGATGATCTCTGCTGCGAATTTGAGCAATTTGATCAACAGAGATC 360

Db 301 GGTTCATCTCAATGGGATGATCTCTGCTGCGAATTTGAGCAATTTGATCAACAGAGATC 360

Qy 361 GAAAGATTCGCAAGAACCCAGGCAATCTCTAGGTTGGAAGATTGAGCAATCTCTACCA 420

Db 361 GAAAGATTCGCAAGAACCCAGGCAATCTCTAGGTTGGAAGATTGAGCAATCTCTACCA 420

Qy 421 ATCTATGCAAGAGCTTCAGAGTGGGAAGCCGATCTTACTTACCACTTCCGCGAG 480

Db 421 ATCTATGCAAGAGCTTCAGAGTGGGAAGCCGATCTTACTTACCACTTCCGCGAG 480

Qy 481 GAAATGCGTATTCATATTCAGCAATGAACAGCGCTTGACACAGCTATCCATTTTC 540

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Qy 1561 GTGAAAGACAGGCTTCAAGAGAGTGAATTTTGAAGAACTTCTCTGCGCAGATT 1620

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Qy 1621 AGCACCCTCAGAGTTTAACTATCCTGACCACTT---TCTCAAGATATGTTGACGATT 1677

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Db	1678	AGAGTTCGTGAGAGTATGCTTCTGTGAC	1737	CCCCCTATTCACCTCAACGTTAATTTGGGGTAAAT	1737	
Qy	1738	CAGGGTAACCTTCTCCGCAACCATGTGCA	1794	--AGCGGACGCAACTTGGCAATCCGGACAGCTTC	1794	
Db	1738	TCATTCGACTTCTCCAAATACAGTTCC	1797	AGACTACAGTACCTCCTTGGAAATATCTCCAAATCC	1797	
Qy	1795	AGAACCGTCGGTTTACACTACCTCTTCA	1854	ATCTCTTAACGATCAAGGGTTTACACCTT	1854	
Db	1798	AGCGATTTCCGTTACTTTGAAAGTCCAA	1857	TGCTTTTACATTTCACTCGGTAAACATCGTG	1857	
Qy	1855	AGCGCTCATGTGTTCAATTCCTGGCA	1914	TGCGCAATGAGTGTACATTTGACCGTATTTGATGTCCT	1914	
Db	1858	GGTGTTAACAACTTATAGTGGACCTG	1917	CAAGAGATTAATTCGACAGATTTGAACTTCATTC	1917	
Qy	1915	CCCCAAGTTACCTTCGAGGCTGAGTACT	1974	GTGAGATTCATGCTGATGTTTGTATGTGATCCTG	1974	
Db	1918	GTTACTCGCAACACTCGAGGCTG---	1974	AAAGAAATTCATGCTGAGATGTTTGTATGATCCTG	1974	
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Qy	2035	TCACAAACGGAACGCAATACAGTTGTG	2094	CGCCATGCAATCTTATACAGATGCAATCAGC	2094	
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Qy	2215	CCCGCTGGCAATATGGAATATGGA	2274	CCATCATTAATCCAGATCTAGCTAAGTTTAG	2274	
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Qy	2275	CAGCGACATCAGGGAACAGTGTAC	2334	ACACCTTACCGTCAAAACCAATTTATGCCGTTA	2334	
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Qy	2395	ATGCTCTGTGCTTGCACGAATAT	2430	TGAGCAAGTAT	2430	
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RESULT 7	AX044385	2062 bp	DNA	linear	PAT 24-NOV-2000	
LOCUS	AX044385	2062 bp	DNA	linear	PAT 24-NOV-2000	
DEFINITION	Sequence 1 from Patent WO0066755.					
ACCESSION	AX044385					
VERSION	AX044385.1					
KEYWORDS	GI:11343263					
SOURCE						
ORGANISM	synthetic construct					
REFERENCE	synthetic construct					
AUTHORS	artificial sequences.					
TITLE	1					
JOURNAL	Christou, P. and Mehlo, L.					
FEATURES	Peptidic fusions					
	Patent: WO 0066755-A 1 09-NOV-2000;					
	Plant Biotechnology Limited (GB)					
	Location/Qualifiers					
	1..2062					
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Query Match	70.0%	Score 1951;	DB 6;	Length 2062;
Best Local Similarity	100.0%	Prod. No. 0;		
Matches 1951;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0
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QY 1921 GTTACCTTGAAGGCTGAGTACTGAGAAATTC 1951
Db 1921 GTTACCTTGAAGGCTGAGTACTGAGAAATTC 1951

RESULT 8
AR110602
LOCUS AR110602 7378 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 9 from patent US 6114608.
ACCESSION AR110602
VERSION AR110602.1 GI:12826878
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 7378)
AUTHORS Mettler, I.J., Dietrich, P.S. and Sinibaldi, R.M.
TITLE Nucleic acid construct comprising bacillus thuringiensis cry1Ab gene
JOURNAL Patent: US 6114608-A 9 05-SEP-2000;
FEATURES
source 1..7378 /organism="unknown"
BASE COUNT 1917 a 1803 c 1719 g 1939 t
ORIGIN
Query Match 66.3%; Score 1848.2; DB 6; Length 7378;
Best Local Similarly 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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 ACCESSION ARI51001
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 JOURNAL Patent: US 6229075-A 9 08-MAY-2001;
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 Best Local Similarity 99.6%; Pred. No. 0;
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 LOCUS AR152424
 DEFINITION Sequence 9 from patent US 6232533.
 ACCESSION AR152424
 VERSION AR152424.1 GI:15118474
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 ORGANISM
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 AUTHORS Mettler, I.J., Platiard, D.C., Griener, S.L., Houghton, W. and Gardiner, M.
 TITLE Inbred maize line R372H
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 VERSION AR184317.1 GI:20228286
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 ORGANISM
 Unknown.
 Unclassified.
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 Mettler, J., Plaisted, D.C., Orler, S.L., Houghton, W. and
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 Best Local Similarity 99.6%; Pred. No. 0;
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Db 1800 TGTCCCACTTACCGAGAAATCTATACCAACCAAGTTCTTGAAGAACTTCCGACGTACT 1859
OY 935 TCCGTGTTCTGCCCCAAGGATTCGAAGGCTCCATCAGAGACCCACACTGTATGACATCT 994
Db 1860 TCCGTGTTCTGCCCCAAGGATTCGAAGGCTCCATCAGAGACCCACACTGTATGACATCT 1919
OY 995 TGAACAGCATTAATCTATCAACCGATGCTCAAGAGAGATTTATCTGTCTGACACC 1054
Db 1920 TGAACAGCATTAATCTATCAACCGATGCTCAAGAGAGATTTATCTGTCTGACACC 1979
OY 1055 AGATCATGGCTCTCCAGTTTGAATTCAGGGGCCGAGTTTACCTTCTCTATGGA 1114
Db 1980 AGATCATGGCTCTCCAGTTTGAATTCAGGGGCCGAGTTTACCTTCTCTATGGA 2039
OY 1115 CTATGGGAAACCGCTCCACAACAGTATGTTGCTCACTAGGTCAGGGTGTCTACA 1174
Db 2040 CTATGGGAAACCGCTCCACAACAGTATGTTGCTCACTAGGTCAGGGTGTCTACA 2099
OY 1175 GAACCTTGTCTTCACCTTGTACAGAAACCTTCAATATCGGTATCAACAACGAGAAC 1234
Db 2100 GAACCTTGTCTTCACCTTGTACAGAAACCTTCAATATCGGTATCAACAACGAGAAC 2159
OY 1235 TTTTCGTTCTTGAACGGAAGATTGCGCTATGGAACCTTCTATCTTGATCCGCTG 1294
Db 2160 TTTTCGTTCTTGAACGGAAGATTGCGCTATGGAACCTTCTATCTTGATCCGCTG 2219
OY 1295 TTTTACGAAAGACGGAACCGTTGATTTCTTGGACGAAATCCCAACGACAAACATG 1354
Db 2220 TTTTACGAAAGACGGAACCGTTGATTTCTTGGACGAAATCCCAACGACAAACATG 2279
OY 1355 TGGCACCCGAGGAGGATTTCTCCACAGTTGAGCCAGTGTCAATGTTCCGTTCCGGAT 1414
Db 2280 TGGCACCCGAGGAGGATTTCTCCACAGTTGAGCCAGTGTCAATGTTCCGTTCCGGAT 2339
OY 1415 TCGACAAAGTTTCGTGAGATCATCAGAGCTCTATGTTCTCATGATTCATCGTAGT 1474
Db 2340 TCGACAAAGTTTCGTGAGATCATCAGAGCTCTATGTTCTCATGATTCATCGTAGT 2399

OY 1475 CTGAGTTCAACAATATCATCTTCTCTCTCAATATCAACCAATCCATTTGACCAAGTTA 1534
Db 2400 CTGAGTTCAACAATATCATCTTCTCTCTCAATATCAACCAATCCATTTGACCAAGTTA 2459
OY 1535 CTAACTTGGATCTGGAACCTTCTGCTGGAAGAACGAGGCTTCAAGAGAGTATATTC 1594
Db 2460 CTAACTTGGATCTGGAACCTTCTGCTGGAAGAACGAGGCTTCAAGAGAGTATATTC 2519
OY 1595 TTAGAAGAACTTCTCTGCGCAGATTTAGCAACCTTCAGAGTTAATCATCTGACCACTTT 1654
Db 2520 TTAGAAGAACTTCTCTGCGCAGATTTAGCAACCTTCAGAGTTAATCATCTGACCACTTT 2579
OY 1655 CTCAAGATATCGTGTCAAGATTGCTTACGATCTTACCACTTACCTTGAATTTCAACCT 1714
Db 2580 CTCAAGATATCGTGTCAAGATTGCTTACGATCTTACCACTTGAATTTCAACCT 2639
OY 1715 CCATTCAGAGGAAGCTTATCAATGAGGTAATCTTCCGGAACCATGTCAGGCGGACGA 1774
Db 2640 CCATTCAGAGGAAGCTTATCAATGAGGTAATCTTCCGGAACCATGTCAGGCGGACGA 2699
OY 1775 ACTTGCAATCCGAGAGCTTCAGAAACCGTCCGTTTCACTACTCTTCAACTTCTTAA 1834
Db 2700 ACTTGCAATCCGAGAGCTTCAGAAACCGTCCGTTTCACTACTCTTCAACTTCTTAA 2759
OY 1835 GATCAAGCGTTTTCACCTTACCGCTCATGTTGTTCAATTTGGCAATGATGATTTG 1894
Db 2760 GATCAAGCGTTTTCACCTTACCGCTCATGTTGTTCAATTTGGCAATGATGATTTG 2819
OY 1895 ACCGATATGAGTTGTGTGCTCCGGAAGTTACCTTCAGAGGAGTACGAAATTCATGC 1954
Db 2820 ACCGATATGAGTTGTGTGCTCCGGAAGTTACCTTCAGAGGAGTACGAAATTCATGC 2879
OY 1955 T 1955
Db 2880 T 2880

RESULT 13
AR212558 7378 bp DNA linear PAT 20-JUN-2002
LOCUS AR212558 Sequence 9 from patent US 6399860.
DEFINITION AR212558
ACCESSION AR212558
VERSION AR212558.1 GI:21516165
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 7378)
AUTHORS Mettler,I.J., Plalsted,D.C., Grier,S.L., Houghton,W. and Gardiner,M.
TITLE Inbred maize line R327H
JOURNAL Patent: US 6399860-A 9 04-JUN-2002;
FEATURES
source 1..7378
BASE COUNT 1917 a 1803 c 1719 g 1939 t
ORIGIN

Query Match 66.3%; Score 1848.2; DB 6; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

OY 95 CCATGACAAACAACCAACATCAAGAAATGCAATTCATCAACCTGTTGAGTAAACCG 154
Db 1020 CCATGACAAACAACCAACATCAAGAAATGCAATTCATCAACCTGTTGAGTAAACCG 1079
OY 155 AAGTTGAATCTTGTGAGAGAACGATTTGAAACCGGTTAAGCTCCATCGACATCTCCT 214
Db 1080 AAGTTGAATCTTGTGAGAGAACGATTTGAAACCGGTTAAGCTCCATCGACATCTCCT 1139
OY 215 TGTCTTGACAGATTTCTGCTCAGCGAGTTGCTGCGAGGTCGAGGTTCTGTTCTCGAC 274

Dh 1140 TGCTTGACACAGTTTCTGCTCAGCGAGTTGTCGACGGTGTGGTCTGCTCGAC 1199
Qy 275 TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGAGATGCAATTCGGTGGCAA 334
Dh 1200 TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGAGATGCAATTCGGTGGCAA 1259
Qy 335 TTGACAGTTGATCAACAGAGATCGAAGATTGCGGAGAACCGACCTCTCTAGT 394
Dh 1260 TTGACAGTTGATCAACAGAGATCGAAGATTGCGGAGAACCGACCTCTCTAGT 1319
Qy 395 TGAAGAGTTGAGCAATCTCAACCAATCTATGAGAGAGCTTCAAGAGTGGGAAAGCG 454
Dh 1320 TGAAGAGTTGAGCAATCTCAACCAATCTATGAGAGAGCTTCAAGAGTGGGAAAGCG 1379
Qy 455 ATCTACTAACCCAGCTCTCCGCGAGAAATGCGATTCAATTGAAACAGATGAAACAGC 514
Dh 1380 ATCTACTAACCCAGCTCTCCGCGAGAAATGCGATTCAATTGAAACAGATGAAACAGC 1439
Qy 515 CTTGACCAACGCTATCCCATTTGTCGAGTCCAGAACTACCAAGTTCTCTTTGCG 574
Dh 1440 CTTGACCAACGCTATCCCATTTGTCGAGTCCAGAACTACCAAGTTCTCTTTGCG 1499
Qy 575 TGTAGTTCAAGCAAGCTAATCTTCAACCTCAGCGTCTCGAGCTTACGCTGTTTGGC 634
Dh 1500 TGTAGTTCAAGCAAGCTAATCTTCAACCTCAGCGTCTCGAGCTTACGCTGTTTGGC 1559
Qy 635 AAAGTGGGAGTTGATGCTGCAACCATCAATAGCCGTTTACAGCACTTACTAGCTGA 694
Dh 1560 AAAGTGGGAGTTGATGCTGCAACCATCAATAGCCGTTTACAGCACTTACTAGCTGA 1619
Qy 695 TTGAAATCTACACGACCAACGCTGTTGTTGATCAACACGCTTGGAGCGTGTCTGG 754
Dh 1620 TTGAAATCTACACGACCAACGCTGTTGTTGATCAACACGCTTGGAGCGTGTCTGG 1679
Qy 755 GTCTGATTTCTAGAGTTGATAGTATCAACAGTTTGAAGAGAAATGACCTGACAG 814
Dh 1680 GTCTGATTTCTAGAGTTGATAGTATCAACAGTTTGAAGAGAAATGACCTGACAG 1739
Qy 815 TTTTGAATTTGATGCTCTCTTCCGGAATATGACTCCAGAACTACCTTCCGTAAG 874
Dh 1740 TTTTGAATTTGATGCTCTCTTCCGGAATATGACTCCAGAACTACCTTCCGTAAG 1799
Qy 875 TGTCCCACTTACAGAGAAATCTATCTAACCCAGTTCTTGAGAACTTGAACGCTAG 934
Dh 1800 TGTCCCACTTACAGAGAAATCTATCTAACCCAGTTCTTGAGAACTTGAACGCTAG 1859
Qy 935 TCCGATGTTCTGCCAAGGTATCGAAGGCTCATAGGAGCCACACTTGAATGACATCT 994
Dh 1860 TCCGATGTTCTGCCAAGGTATCGAAGGCTCATAGGAGCCACACTTGAATGACATCT 1919
Qy 995 TGAACAGATTAATCTATCTACACCGATGCTCAAGAGAGATATTACTGTCTGACACC 1054
Dh 1920 TGAACAGATTAATCTATCTACACCGATGCTCAAGAGAGATATTACTGTCTGACACC 1979
Qy 1055 AGATCATGAGCTTCTTCAGTTGATTCAGCGGCGCCGAGTTTACCTTTCTCTATGAA 1114
Dh 1980 AGATCATGAGCTTCTTCAGTTGATTCAGCGGCGCCGAGTTTACCTTTCTCTATGAA 2039
Qy 1115 CTATGAGGAAACGCGCTCCACAAACAGATGCTCAACTAGAGGTGATCTTCA 1174
Dh 2040 CTATGAGGAAACGCGCTCCACAAACAGATGCTCAACTAGAGGTGATCTTCA 2099
Qy 1175 GAACCTGTCTTCAACCTTGTATCAGAAAGACCTTCAATATCGGTATCAACACAGCAAC 1234
Dh 2100 GAACCTGTCTTCAACCTTGTATCAGAAAGACCTTCAATATCGGTATCAACACAGCAAC 2159
Qy 1235 TTTCCGTTCTTGAAGGAAACAGAGTTGCTTATGAACTTTTCTTACTTGGATCCGCTG 1294
Dh 2160 TTTCCGTTCTTGAAGGAAACAGAGTTGCTTATGAACTTTTCTTACTTGGATCCGCTG 2219
Qy 1295 TTTACAGAAAGAGCGGAAACGTTGATCTTGAAGAAATCCACCAAGAAACATG 1354
Dh 2220 TTTACAGAAAGAGCGGAAACGTTGATCTTGAAGAAATCCACCAAGAAACATG 2279

Qy 1355 TGCCACCAGCAAGATTTCTCCACAGGTTGACCAAGTGTCCATGTTCCGTTCCGAT 1414
Dh 2280 TGCCACCAGCAAGATTTCTCCACAGGTTGACCAAGTGTCCATGTTCCGTTCCGAT 2339
Qy 1415 TCAGCAACAGTTCCGTGAGCATCATGAGGCTCTATGTTCTCATGATTTATGTAGT 1474
Dh 2340 TCAGCAACAGTTCCGTGAGCATCATGAGGCTCTATGTTCTCATGATTTATGTAGT 2399
Qy 1475 CTGAGTTCAACCAATATCTTCTTCCCTCAATACCCCAAAATCCATTTGACCAAGTCTA 1534
Dh 2400 CTGAGTTCAACCAATATCTTCTTCCCTCAATACCCCAAAATCCATTTGACCAAGTCTA 2459
Qy 1535 CTAACTTGAATCTGAACTTCTGTGCTGTAAGAGACAGGCTTCAAGAGATGATATTC 1594
Dh 2460 CTAACTTGAATCTGAACTTCTGTGCTGTAAGAGACAGGCTTCAAGAGATGATATTC 2519
Qy 1595 TTGAAAGAACTTCTCTGCGCAATTTAGCAACCTCAGAGTTTACATCATCTGACACCTT 1654
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Qy 1655 CTGAAGATATCGTGCAGAGTTGTTAGCATCTTACCACTTACCTTCAATTTCCACACT 1714
Dh 2580 CTGAAGATATCGTGCAGAGTTGTTAGCATCTTACCACTTACCTTCAATTTCCACACT 2639
Qy 1715 CCATGACGGAAGGCTATCATCAGGATTAATTTCTCCGAACCATGTCAAGCGGACGA 1774
Dh 2640 CCATGACGGAAGGCTATCATCAGGATTAATTTCTCCGAACCATGTCAAGCGGACGA 2699
Qy 1775 ACTTGCAATCGGAGAGCTTCAAGAACGTCGTTTCACTGCTTTCAACTTCTCTAAC 1834
Dh 2700 ACTTGCAATCGGAGAGCTTCAAGAACGTCGTTTCACTGCTTTCAACTTCTCTAAC 2759
Qy 1835 GATCAAGGTTTTCACCTTAGCGCTCATGTTCAATTTCTGGAATGAAGTGTACATTTG 1894
Dh 2760 GATCAAGGTTTTCACCTTAGCGCTCATGTTCAATTTCTGGAATGAAGTGTACATTTG 2819
Qy 1895 ACCGATTTGATTTGTGCTCCGCAAGTTTACCTTCAAGGCTGAGTACTGAAATTCATGC 1954
Dh 2820 ACCGATTTGATTTGTGCTCCGCAAGTTTACCTTCAAGGCTGAGTACTGAGATTCAGGA 2879
Qy 1955 T 1955
Dh 2880 T 2880

RESULT 14
AR110596
LOCUS AR110596 1851 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6114608.
ACCESSION AR110596
VERSION AR110596.1 GI:12826872
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1851)
AUTHORS Mettler,I.J., Dietrich,P.S. and Sinibaldi,R.M.
TITLE Nucleic acid construct comprising bacillus thuringiensis cryIab gene
JOURNAL Patent: US 6114608-A 3 05-SEP-2000;
FEATURES
source location/Qualifiers
1..1851
BASE COUNT 478 a 504 c 394 g 475 t
ORIGIN
Query Match 66.2%; Score 1845.4; DB 6; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 96 CATGACAAACCAACCAATCAAGATGATTCATCAATGCTTGAATACCCAGA 155

Db 1 CATTGACACAAACCAACATCAAGAAATGATTCATACATCTGCTTGAATTAACCA 60
 Qy 156 AGTTGAAGTACTTGGTGAAGAACGATGAAACCGGTTACATCCCATCTGCTT 215
 Db 61 AGTTGAAGTACTTGGTGAAGAACGATGAAACCGGTTACATCCCATCTGCTT 120
 Qy 216 GTCTTGAACACAGTTTCTGCTGAGGAGTTCTGTCAGAGTCTGAGGTTCTGCTGAG 275
 Db 121 GTCTTGAACACAGTTTCTGCTGAGGAGTTCTGTCAGAGTCTGAGGTTCTGCTGAG 180
 Qy 276 AGTTGAAGTACTTGGTGAAGAACGATGAAACCGGTTACATCCCATCTGCTTGA 335
 Db 181 AGTTGAAGTACTTGGTGAAGAACGATGAAACCGGTTACATCCCATCTGCTTGA 240
 Qy 336 TGAGCAGTTGATCAACAGAGATGAAAGATTCGCGAGAAACGAGGCATCTGAGTT 395
 Db 241 TGAGCAGTTGATCAACAGAGATGAAAGATTCGCGAGAAACGAGGCATCTGAGTT 300
 Qy 396 GGAAGATTTGAGCAATCTTCAACAAATCTATGACAGAGCTTCAGAGAGTGGAAAG 455
 Db 301 GGAAGATTTGAGCAATCTTCAACAAATCTATGACAGAGCTTCAGAGAGTGGAAAG 360
 Qy 456 TCCCTACTAACCCAGTCTCTCCGAGGAAATGCGTATTTCAATTCACACGATGAAC 515
 Db 361 TCCCTACTAACCCAGTCTCTCCGAGGAAATGCGTATTTCAATTCACACGATGAAC 420
 Qy 516 CTTGACACAGCTATCCCATTTGTTGCGAGTCCAGAACCTACCAAGTTCTCTGCTG 575
 Db 421 CTTGACACAGCTATCCCATTTGTTGCGAGTCCAGAACCTACCAAGTTCTCTGCTG 480
 Qy 576 GTACGTTCAAGCAAGTAACTTTCACTCAGCGTCTTCAAGAGCTTGAAGCTGTTGG 635
 Db 481 GTACGTTCAAGCAAGTAACTTTCACTCAGCGTCTTCAAGAGCTTGAAGCTGTTGG 540
 Qy 636 AAGTGGGAGTTTCAATGCTGGAACCAATAGCCGTTACACAGCTTACTAGGCTGAT 695
 Db 541 AAGTGGGAGTTTCAATGCTGGAACCAATAGCCGTTACACAGCTTACTAGGCTGAT 600
 Qy 696 TGAACACTACACCGACAGCTGTTGTTGTTACACACAGCTTGAAGCTGTTGGG 755
 Db 601 TGAACACTACACCGACAGCTGTTGTTGTTACACACAGCTTGAAGCTGTTGGG 660
 Qy 756 TCCGATTTCTAGAGTTGATTTAGTATACCAACGATTCAGAGAGATTTGACCTTCA 815
 Db 661 TCCGATTTCTAGAGTTGATTTAGTATACCAACGATTCAGAGAGATTTGACCTTCA 720
 Qy 816 TTTGACATTTGTTCTCTTCCGACATTAAGCTCCGAACTTACCTTATCCGACAGT 875
 Db 721 TTTGACATTTGTTCTCTTCCGACATTAAGCTCCGAACTTACCTTATCCGACAGT 780
 Qy 876 GTCCCACTTACAGAGAAATCTATACCTAACCCAGTTCTTGAAGATTCGACGTAAGT 935
 Db 781 GTCCCACTTACAGAGAAATCTATACCTAACCCAGTTCTTGAAGATTCGACGTAAGT 840
 Qy 936 CCGTGGTTCTGCGCAAGGTTATGAAAGCTTCATCAGAGCCCACTTGTATGACATTT 995
 Db 841 CCGTGGTTCTGCGCAAGGTTATGAAAGCTTCATCAGAGCCCACTTGTATGACATTT 900
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 Db 961 GATCATGAGCTCTCAGTTGATTTGAGGAGGCGCCGAGTTTACCTTCTCTATGAAAC 1020
 Qy 1116 TATGGGAAACCGCGCTTCAACAAAGTATCGTTCTCACTAGTCAAGGCTTCAAG 1175
 Db 1021 TATGGGAAACCGCGCTTCAACAAAGTATCGTTCTCACTAGTCAAGGCTTCAAG 1080
 Qy 1176 AACCTGTCTTCCAGCTTGTACAGAGACCTTCAATTCGCTATCAACCAACAGCACT 1235
 Db 1081 AACCTGTCTTCCAGCTTGTACAGAGACCTTCAATTCGCTATCAACCAACAGCACT 1140

Qy 1236 TTCGTTCTTACAGGAAACAGAGTTCCGCTATGAAACCTTCTTAACTTGGCTATCCGCTG 1295
 Db 1141 TTCGTTCTTACAGGAAACAGAGTTCCGCTATGAAACCTTCTTAACTTGGCTATCCGCTG 1200
 Qy 1296 TTAAGAAAGAGCGGAAACCGTTGATTTCTTGGAGGAAATCCCAACAGAAACAAATGT 1355
 Db 1201 TTAAGAAAGAGCGGAAACCGTTGATTTCTTGGAGGAAATCCCAACAGAAACAAATGT 1260
 Qy 1356 GCCACCCAGGCAAGAGATTTCTCCCAAGTTGAGCCAGTGTCCATGTTCCGTTCCGATT 1415
 Db 1261 GCCACCCAGGCAAGAGATTTCTCCCAAGTTGAGCCAGTGTCCATGTTCCGTTCCGATT 1320
 Qy 1416 CAGCAACAGTTCCGTAAGCATCATCAGAGCTCTATGTTCTATGATTCATCTGATGTC 1475
 Db 1321 CAGCAACAGTTCCGTAAGCATCATCAGAGCTCTATGTTCTATGATTCATCTGATGTC 1380
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 Db 1381 TGAATTAACATATCATTTCTTCTCTTCAATTAACCAAAATCCCATTTGACCAAGTCTAC 1440
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 Db 1501 TAGAAGAACTTCTCTGCGCAGATTTAGACACCTTCAAGATTAACATCACTGACCACTTC 1560
 Qy 1656 TCAAGATATCTGTCAGAGATTTCTTACGATTCACCACTTAATTTGCAATTCACACTC 1715
 Db 1561 TCAAGATATCTGTCAGAGATTTCTTACGATTCACCACTTAATTTGCAATTTCCACACTC 1620
 Qy 1716 CATGACGAAAGGCTTCAATCAGAGTAACTTCTCCGCAACATGTCAAGCGCAGCAA 1775
 Db 1621 CATGACGAAAGGCTTCAATCAGAGTAACTTCTCCGCAACATGTCAAGCGCAGCAA 1680
 Qy 1776 CTTGCAATTCGCGAGCTTCAGAACCGTCTGCTTCACTACTCTTTCATCTTCTTAA 1835
 Db 1681 CTTGCAATTCGCGAGCTTCAGAACCGTCTGCTTCACTACTCTTTCATCTTCTTAA 1740
 Qy 1836 ATCAAGGTTTTCACCTTACGCTCATGTTGTTCAATTTGCGCAATGAAGTGTACATTTGA 1895
 Db 1741 ATCAAGGTTTTCACCTTACGCTCATGTTGTTCAATTTGCGCAATGAAGTGTACATTTGA 1800
 Qy 1896 CCGTATTGAGTTTGTGCTGCGGAAATTAACCTTGAAGCTGAGTACT 1942
 Db 1801 CCGTATTGAGTTTGTGCTGCGGAAATTAACCTTGAAGCTGAGTACT 1847

RESULT 15
 ARI50995 1851 bp DNA linear PAT 08-AUG-2001
 LOCUS ARI50995
 DEFINITION Sequence 3 from parent US 6229075.
 ACCESSION ARI50995
 VERSION ARI50995.1 GI:15115586
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown.
 REFERENCE
 1 (bases 1 to 1851)
 Mettler, J., Plaisted, D.C., Grier, S.L., Houghton, W. and
 Gardiner, M.
 TITLE
 JOURNAL
 Patent: US 6229075-A 3 08-MAY-2001;
 FEATURES
 source
 1..1851
 /organism="unknown"
 BASE COUNT 478 a 504 c 394 g 475 t
 ORIGIN
 Query Match 66.2%; Score 1845.4; DB 6; Length 1851;
 Best local Similarity 99.9%; Pred. No. 0;

Matches	1846;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	96	CATGACACAAACCCAAACATCAACGATGATTCATACAACTGCTTGAGTAAACCGAGA	155						
Db	1	CATGACACAAACCCAAACATCAACGATGATTCATACAACTGCTTGAGTAAACCGAGA	60						
Qy	156	AGTTGAAGTACTTGCTGGAGAAACGATTTGAAACCGGTTACACTCCCATCGACATCTCTT	215						
Db	61	AGTTGAAGTACTTGCTGGAGAAACGATTTGAAACCGGTTACACTCCCATCGACATCTCTT	120						
Qy	216	GTCCTTGACACAGTTTCTGCTCAGAGAGTTGCTGCAGAGTCTGGGTTCTGCTTCGAGCT	275						
Db	121	GTCCTTGACACAGTTTCTGCTCAGAGAGTTGCTGCAGAGTCTGGGTTCTGCTTCGAGCT	180						
Qy	276	AGTTGACATCATCTGGGGTATCTTTGCTCATCTCAATGGAGTGCATCTCTGTCGAAT	335						
Db	181	AGTTGACATCATCTGGGGTATCTTTGCTCATCTCAATGGAGTGCATCTCTGTCGAAT	240						
Qy	336	TGACAGTTGATCAACCAAGAGATCGAAGAGTTGCGCAGAAACCAAGCCATCTAGGTT	395						
Db	241	TGACAGTTGATCAACCAAGAGATCGAAGAGTTGCGCAGAAACCAAGCCATCTAGGTT	300						
Qy	396	GGAAGGATGTGAGCATCTCTCAACATCTATGACAGAGCTTCAAGAGTGGGAAGCCGA	455						
Db	301	GGAAGGATGTGAGCATCTCTCAACATCTATGACAGAGCTTCAAGAGTGGGAAGCCGA	360						
Qy	456	TCCTACTAACCCAGCTCTCCGCGAGGAAGTCTGATTCATTCATCAACGATGAAACAGCGC	515						
Db	361	TCCTACTAACCCAGCTCTCCGCGAGGAAGTCTGATTCATTCATCAACGATGAAACAGCGC	420						
Qy	516	CTTGAACACAGCTATCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTCTTGTCCGT	575						
Db	421	CTTGAACACAGCTATCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTCTTGTCCGT	480						
Qy	576	GTACGTTCAACAGCATATCTTCAACCTGAGGCTGTTGAGACGTTAGCGTTTGAGCA	635						
Db	481	GTACGTTCAACAGCATATCTTCAACCTGAGGCTGTTGAGACGTTAGCGTTTGAGCA	540						
Qy	636	AAGGTGGGATTCGATGCTGCAACCATCAATAGCCGTTTACAAACGACCTTATAGGCTGAT	695						
Db	541	AAGGTGGGATTCGATGCTGCAACCATCAATAGCCGTTTACAAACGACCTTATAGGCTGAT	600						
Qy	696	TGAAACATCAACCCGACCGCTGTTGCTTGGTGAACAACCTGCTTGAAGCGTGTGGGG	755						
Db	601	TGAAACATCAACCCGACCGCTGTTGCTTGGTGAACAACCTGCTTGAAGCGTGTGGGG	660						
Qy	756	TCCTGATCTAGAGTTGGATTGATTAACAACAGTTGAGAGAAATTGACCCCTACAGT	815						
Db	661	TCCTGATCTAGAGTTGGATTGATTAACAACAGTTGAGAGAAATTGACCCCTACAGT	720						
Qy	816	TTTGGACATTTGCTCTCTTCCGAACTATGACTCGAAGCTTACCTTATCCGTAAGT	875						
Db	721	TTTGGACATTTGCTCTCTTCCGAACTATGACTCGAAGCTTACCTTATCCGTAAGT	780						
Qy	876	GTCCCAATTTACACAGAAATCTATACTAACCCAGTCTTTGAGAACTTGCAGCGTACCTT	935						
Db	781	GTCCCAATTTACACAGAAATCTATACTAACCCAGTCTTTGAGAACTTGCAGCGTACCTT	840						
Qy	936	CCGTGCTTCTGCGCCAAAGGATTCGAAGGCTCCATCGAGAGCCACACTTGATGACATCTT	995						
Db	841	CCGTGCTTCTGCGCCAAAGGATTCGAAGGCTCCATCGAGAGCCACACTTGATGACATCTT	900						
Qy	996	GAACAGATTAATCTATCTACACGATGCTCAACAGAGAGATTTACTGCTGACACCA	1055						
Db	901	GAACAGATTAATCTATCTACACGATGCTCAACAGAGAGATTTACTGCTGACACCA	960						
Qy	1056	GATCATGCGCTTCCAGTTGATTTCAAGCGGCGCCAGATTACCTTCTCTCTATGGAAC	1115						
Db	961	GATCATGCGCTTCCAGTTGATTTCAAGCGGCGCCAGATTACCTTCTCTCTATGGAAC	1020						
Qy	1116	TATGGAAAGCGCGCTCCACAAACAGATCTGTTGCTCAACTAGGTCAGGGGTGTCTACAG	1175						
Db	1021	TATGGAAAGCGCGCTCCACAAACAGATCTGTTGCTCAACTAGGTCAGGGGTGTCTACAG	1080						

Qy	1176	AACCTTGTCTTCCACTTGTGACAGAGACCCCTTCAATATGCTATCAACCAACGACCACT	1235
Db	1081	AACCTTGTCTTCCACTTGTGACAGAGACCCCTTCAATATGCTATCAACCAACGACCACT	1140
Qy	1236	TTCCGCTTCTTGAACGGAACAGAGTTCCGCTTATGAAACCTCTTCTAATCTTGCCATCCGCTG	1295
Db	1141	TTCCGCTTCTTGAACGGAACAGAGTTCCGCTTATGAAACCTCTTCTAATCTTGCCATCCGCTG	1200
Qy	1296	TTACAGAAAGAGCCGAACCGTTGATTCCTTGAAGAAATCCACACAGAAACCAATATG	1355
Db	1201	TTACAGAAAGAGCCGAACCGTTGATTCCTTGAAGAAATCCACACAGAAACCAATATG	1260
Qy	1356	GCCACCCAGGCAAGAGATTCCTCCAACAGTTGAGCCACAGTGTCCATGTTCCGTTCCGATT	1415
Db	1261	GCCACCCAGGCAAGAGATTCCTCCAACAGTTGAGCCACAGTGTCCATGTTCCGTTCCGATT	1320
Qy	1416	CAGCAACAGTTCCGCTGACATCATCAGAGCTCCATATGTTCTCATGATTTCAATCGTAGTGC	1475
Db	1321	CAGCAACAGTTCCGCTGACATCATCAGAGCTCCATATGTTCTCATGATTTCAATCGTAGTGC	1380
Qy	1476	TGAGTTCAACAAATATCATTCCTTCTCTCAAAATCAACCAATCCCATTTGACCAAGTCTAC	1535
Db	1381	TGAGTTCAACAAATATCATTCCTTCTCTCAAAATCAACCAATCCCATTTGACCAAGTCTAC	1440
Qy	1536	TAACTTGGATCTGGAACCTTCTGTGTGAAAGAACCAAGCTTCAACAGAGGTGATATTCT	1595
Db	1441	TAACTTGGATCTGGAACCTTCTGTGTGAAAGAACCAAGCTTCAACAGAGGTGATATTCT	1500
Qy	1596	TAGAAGAACTTCTCTGCGCCAGATTAGCAACCTCAGAGTTTAAACATCACTGACCACTTTC	1655
Db	1501	TAGAAGAACTTCTCTGCGCCAGATTAGCAACCTCAGAGTTTAAACATCACTGACCACTTTC	1560
Qy	1656	TCAAAGATATGCTGACAGATTCGTTACGATCTACCACTTAACTTGCACACCTC	1715
Db	1561	TCAAAGATATGCTGACAGATTCGTTACGATCTACCACTTAACTTGCACACCTC	1620
Qy	1716	CATGACGGAAGGCTTATCAATCAAGGTTAATCTTCCGCAACCATGTCAGCGGACGAA	1775
Db	1621	CATGACGGAAGGCTTATCAATCAAGGTTAATCTTCCGCAACCATGTCAGCGGACGAA	1680
Qy	1776	CTTGCAATCCGGCAGCTTACGAACCGTCCGTTTCACTACTCTTCAACTCTCTAACGG	1835
Db	1681	CTTGCAATCCGGCAGCTTACGAACCGTCCGTTTCACTACTCTTCAACTCTCTAACGG	1740
Qy	1836	ATCAAGGCTTTTCAACCTTAGCGCTCATGTTGTTCAATTTCTGCAATGAAGTATCATTTGA	1895
Db	1741	ATCAAGGCTTTTCAACCTTAGCGCTCATGTTGTTCAATTTCTGCAATGAAGTATCATTTGA	1800
Qy	1896	CCGTATTGAGTTTGTGCTGCGCAAGTTTACCTTGAAGCTGAGTACT	1942
Db	1801	CCGTATTGAGTTTGTGCTGCGCAAGTTTACCTTGAAGCTGAGTACT	1847

Search completed: October 21, 2003, 09:43:20
 Job time : 9921 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 21, 2003, 05:00:28 ; Search time 706 Seconds

(without alignments)
10660.104 Million cell updates/sec

Title: US-09-980-650-6

Perfect score: 2788
Sequence: 1 aaataagcattctactgctt.....tactagagacatcatcag 2788

Scoring table: IDENTITY NUC
Gapop 10%0, Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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24: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*
25: /SIDSI/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2788	100.0	2788	22	AAA88919
2	2659.4	95.4	2692	22	AAA88920
3	2407.6	86.4	2436	22	AAA88921
4	2333.2	83.7	2788	22	AAA88922
5	2204.6	79.1	2692	22	AAA88923
6	1952.8	70.0	2436	22	AAA88924
7	1951	70.0	2062	22	AAA88914
8	1848.2	66.3	7378	21	AAA75466

9	1848.2	66.3	7378	22	AA06314	Plasmid p201502 co
10	1848.2	66.3	7378	22	AA06368	Plasmid p201502 co
11	1848.2	66.3	7378	22	AA89825	Nucleotide sequenc
12	1848.2	66.3	7378	22	AA89834	Nucleotide sequenc
13	1848.2	66.3	7378	24	AB157460	Plasmid p201502 en
14	1845.4	66.2	1851	21	AAA75460	Nucleotide sequenc
15	1845.4	66.2	1851	22	AA06308	Insecticidal CryIA
16	1845.4	66.2	1851	22	AA06362	Insecticidal CryIA
17	1845.4	66.2	1851	22	AA06362	Nucleotide sequenc
18	1845.4	66.2	1851	22	AA89828	Nucleotide sequenc
19	1845.4	66.2	1851	24	AB157434	CryIab crystal pro
20	1845	66.2	1845	11	AA05792	Encodes modified B
21	1845	66.2	1845	20	AA231666	Artificially modif
22	1844.8	66.2	3484	19	AAV00355	Insecticidal gene
23	1844.8	66.2	3484	22	AAV00355	Modified Bacillus
24	1843.8	66.1	1851	22	AA06373	CryIab toxin DNA o
25	1843.4	66.1	3531	19	AAV00293	Bacillus thuringie
26	1843.4	66.1	3531	22	AAV03209	Modified Bacillus
27	1838.6	65.9	3531	22	AA508961	B.t.k. HD-73/HD-1
28	1837	65.9	1845	22	AA508947	Bacillus thuringie
29	1507.8	54.1	2062	22	AA88915	Nucleotide sequenc
30	1416.2	50.8	1962	21	AAZ59084	B. thuringiensis C
31	1411.8	50.6	1920	11	AA005793	Encodes modified B
32	1411.8	50.6	1920	22	AA508955	Bacillus thuringie
33	1411.8	50.6	3534	11	AA005794	Encodes modified B
34	1411.8	50.6	3534	11	AA005795	Encodes full-length
35	1411.8	50.6	3534	22	AA006561	Encodes full-length
36	1411.8	50.6	3534	11	AA508957	Bacillus thuringie
37	1411.8	50.6	3534	22	AA508960	B.t.k. fully synth
38	1407	50.5	3534	22	AA508959	B.t.k. synthetic f
39	1392.6	49.9	3478	19	AAV00291	Insecticidal prote
40	1392.6	49.9	3478	22	AAV03207	Modified Bacillus
41	1328.8	47.7	1767	22	AA508953	Bacillus thuringie
42	1325.6	47.5	1767	11	AA005791	Encodes modified B
43	1322	43.8	4360	10	AAV05094	Chimeric gene codi
44	1220.4	43.8	2815	11	AA004024	Gene p412 encoding
45	1220.4	43.8	3066	11	AA004025	Gene p412 encoding

ALIGNMENTS

RESULT 1	
AAA88919	AAA88919 standard; DNA; 2788 BP.
ID	AAA88919
XX	AAA88919;
AC	
XX	
DT	05-MAR-2001 (first entry)
XX	
DE	Nucleotide sequence of CryIA(b)-RTB1 fusion in pFASTBAC1.
XX	
KW	CryIA(b); crystal protein; ricin toxin B; RTB1; lectin;
KW	insecticide; pesticide; toxin; transgenic plant; insect resistance;
KW	crop protection; pFASTBAC1; ds.
XX	
OS	Chimeric - Bacillus thuringiensis.
OS	Chimeric - Ricinus communis.
OS	Chimeric - Baculovirus.
XX	
XX	WO200066755-A2.
XX	
XX	09-NOV-2000.
PD	
XX	
PF	27-APR-2000; 2000WO-GB01633.
XX	
PR	28-APR-1999; 99GB-0009796.
XX	
PA	(PLAN-) PLANT BIOSCIENCE LTD.
XX	
PI	Christou P, Menlo L;
XX	
DR	WPI: 2001-007228/01.

QY 1741 GGTAACTTCTCCGCAACCATGTCAAGCGGCAACCTTGCAATCCGCGAGCTTGAGAAC 1800
 DB 1741 GGTAATCTCTCCGCAACCATGTCAAGCGGCAACCTTGCAATCCGCGAGCTTGAGAAC 1800
 QY 1801 GTGGTTTCACTACCTCTTCAAGCTTCTTAAGGGATCAAGCGTTTTCACCTTAGGCT 1860
 DB 1801 GTGGTTTCACTACCTCTTCAAGCTTCTTAAGGGATCAAGCGTTTTCACCTTAGGCT 1860
 QY 1861 CATGTGTTCAATTCGTGCAATGAAGTGACATTGACCGTATGATGTTTGTGCTGCGAA 1920
 DB 1861 CATGTGTTCAATTCGTGCAATGAAGTGACATTGACCGTATGATGTTTGTGCTGCGAA 1920
 QY 1921 GTTACCTTGAAGCTGAGTACTGAGAAATTCATGCTGATGTTTGTATGATCTTGAGCCCA 1980
 DB 1921 GTTACCTTGAAGCTGAGTACTGAGAAATTCATGCTGATGTTTGTATGATCTTGAGCCCA 1980
 QY 1981 TAGTCCGATGTAGTGTGAAATGCTATGATGTTTGTATGATGTTTGTATGATGTTTGTATG 2040
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 QY 2041 ACGGAAACGCAATACAGTTGTGCGCATGCAAGTCTATATACAGATGCAAAATCAGCTTGA 2100
 DB 2041 ACGGAAACGCAATACAGTTGTGCGCATGCAAGTCTATATACAGATGCAAAATCAGCTTGA 2100
 QY 2101 CTTTGAAGAAAGACAACTATCTATGATCTTAATGCAAAAGTGTTTAACTTACGGGTACA 2160
 DB 2101 CTTTGAAGAAAGACAACTATCTATGATCTTAATGCAAAAGTGTTTAACTTACGGGTACA 2160
 QY 2161 GTCCGGGAGTCTATGATGATGATCTATGATGATGATGATGATGATGATGATGATGATGATG 2220
 DB 2161 GTCCGGGAGTCTATGATGATGATCTATGATGATGATGATGATGATGATGATGATGATGATG 2220
 QY 2221 GGCAAATATGSGATATGATGAAACCATCATMAATCCAGATCTAGTCTAGTTTGAAGCGGA 2280
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 QY 2281 CATCAGGGAACAGTGTATACACACTTACGCTGCAAAACCAACATTTATCCCTTACTAGTCAAG 2340
 DB 2281 CATCAGGGAACAGTGTATACACACTTACGCTGCAAAACCAACATTTATCCCTTACTAGTCAAG 2340
 QY 2341 GTTGGCTTCTTAATTAATACAAACCTTTTGTACAAACCACTGTTGGGCTATATGCTC 2400
 DB 2341 GTTGGCTTCTTAATTAATACAAACCTTTTGTACAAACCACTGTTGGGCTATATGCTC 2400
 QY 2401 TGTGCTTCAAGCAAAATAGTGAGCAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG 2460
 DB 2401 TGTGCTTCAAGCAAAATAGTGAGCAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATG 2460
 QY 2461 AACCAAGTGGGCTCTTTATGAGATGTTGTTCAATCGTCTGAGCAAAACCGAGTAATTT 2520
 DB 2461 AACCAAGTGGGCTCTTTATGAGATGTTGTTCAATCGTCTGAGCAAAACCGAGTAATTT 2520
 QY 2521 GCGTTACAGTATCTTAATATAGCGGAAACGTTTAAAGTCTCTGTTGGCCCTG 2580
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 QY 2581 CATCCTCTGCGCAACGATGATGTTCAAGATGATGGAACCAATTTAAATTTGTAATG 2640
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 DB 2641 GATTGGTGTAGATGTGAGGCGATGCGATCCGAGCTTAAACAAATCATTTCTTTACCTC 2700
 QY 2701 TCCATGTGTGACCCCAACCAATATGTTTACATTTATTTGATGACAGATTTCAAGCTTG 2760
 DB 2701 TCCATGTGTGACCCCAACCAATATGTTTACATTTATTTGATGACAGATTTCAAGCTTG 2760
 QY 2761 TCGAAGATCTAGAGATCATTAATCAG 2788
 DB 2761 TCGAAGATCTAGAGATCATTAATCAG 2788

RESULT 2
 ID AAA88920 standard; DNA; 2692 BP.
 AC AAA88920;
 XX 05-MAR-2001 (first entry)
 DE Nucleotide sequence of CryIA(b)-RTB2 fusion in pRSTBAC1.
 XX
 KM CryIA(b): crystal protein; ricin toxin B; RTB2; lectin;
 KM insecticide; pesticide; toxin; transgenic plant; insect resistance;
 KM crop protection; pRSTBAC1; ds.
 XX
 OS Chimeric - Bacillus thuringiensis.
 OS Chimeric - Ricinus communis.
 OS Chimeric - Baculovirus.
 XX W020006755-A2.
 XX
 XX 09-NOV-2000.
 PD
 XX 27-APR-2000; 2000WO-GB01633.
 PF
 XX 28-APR-1999; 99GB-0009796.
 PR
 XX (PLAN-) PLANT BIOSCIENCE LTD.
 PA
 XX
 PI Christou P, Mehlo L;
 XX WPI; 2001-007226/01.
 DR
 XX
 PT Novel nucleic acid molecule encoding a pesticidal fusion polypeptide
 PT comprising a toxin and a binding domain for producing transgenic plants
 PT resistant to pests -
 XX
 XX Claim 11; Fig 3g; 81pp; English.
 PS
 CC This nucleotide sequence is that of a fusion between DNA encoding
 CC crystal protein CryIA(b) (see AAA88914) of *Bacillus thuringiensis* and
 CC DNA encoding ricin toxin B RTB2 (see AAA88917) in baculovirus transfer
 CC vector pRSTBAC1, in which the fusion was cloned under the control
 CC of the polyhedrin promoter. This is an example of claimed nucleic
 CC acids encoding pesticidal fusion proteins between a toxin domain
 CC and a heterologous binding domain capable of binding non-specifically
 CC to a cell membrane without disrupting that membrane. The use of such
 CC fusions may help to inhibit the acquisition of resistance in a pest
 CC population treated with the protein. Vectors (e.g. baculovirus
 CC vectors or vectors suitable for use in a plant) are also provided.
 CC Transgenic plants (especially rice or maize) are also provided.
 CC Expression of the fusion protein in a plant is useful for influencing
 CC or affecting the toxicity of a plant to a pest, allowing control of
 CC e.g. Lepidoptera, Coleoptera, Culicidae, Simuliidae, Hymenoptera,
 CC Homoptera, Diptera and Orthoptera pests.
 XX
 SQ Sequence 2692 BP; 730 A; 660 C; 586 G; 716 T; 0 other;
 Query Match 95.4%; Score 2659.4; DB 22; Length 2692;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2660; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 AAATAGATTTTACTGTTTCTGTAACAGTTTGTATATATATATATATATATATATATATATAT 60
 DB 1 AAATAGATTTTACTGTTTCTGTAACAGTTTGTATATATATATATATATATATATATATATAT 60
 QY 61 GATTATTCATCCGTCACCATGCGGGGCGGATCCATGCAACCAACCAACCAACCAACCAACCAAC 120
 DB 61 GATTATTCATCCGTCACCATGCGGGGCGGATCCATGCAACCAACCAACCAACCAACCAACCAAC 120
 QY 121 GAATGCATTCATCAACCTGCTTGAATACCCAGAAAGTTGAAGTCTTGTGTGAGAAAGC 180
 DB 121 GAATGCATTCATCAACCTGCTTGAATACCCAGAAAGTTGAAGTCTTGTGTGAGAAAGC 180

QY 181 ATTGAAACCGGTTACACTCCCATCGACATCTCCTTGTCTTGACACAGTTTCTGCTGAC 240
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Db 181 ATTGAAACCGGTTACACTCCCATCGACATCTCCTTGTCTTGACACAGTTTCTGCTGAC 240
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QY 241 GAGTTCGTCAGAGTGCTGGGTGTTCTCGGACTAGTGAATCATCTGGGGATCTTT 300
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Db 241 GAGTTCGTCAGAGTGCTGGGTGTTCTCGGACTAGTGAATCATCTGGGGATCTTT 300
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QY 301 GGTCCATCTCAATGGGATGATCTCCTGGTGCAAAATTGACAGTTGATCAACAGAGATC 360
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Db 301 GGTCCATCTCAATGGGATGATCTCCTGGTGCAAAATTGACAGTTGATCAACAGAGATC 360
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QY 361 GAAAGATTGCGCAGAGAACAGGCCATCTTAGTTGGAAGATTGAGCAATCTCTACAA 420
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Db 361 GAAAGATTGCGCAGAGAACAGGCCATCTTAGTTGGAAGATTGAGCAATCTCTACAA 420
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QY 421 ATCTATGAGAGAGCTTCAGAGAGTGGGAAGCCCATCTACTAACCCGAGCTCCGAG 480
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Db 421 ATCTATGAGAGAGCTTCAGAGAGTGGGAAGCCCATCTACTAACCCGAGCTCCGAG 480
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QY 481 GAAATGCGTATTTCAATTCAAGACATGAACAGCGCTTGACACAGCTATCCATTTGTC 540
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Db 481 GAAATGCGTATTTCAATTCAAGACATGAACAGCGCTTGACACAGCTATCCATTTGTC 540
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Db 841 AACTATGACTCCAGAACCTTACCCTATCCGTACAGTGTCCCACTTACAGAGAAATCTAT 900
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Db 901 ACTAACCCAGTTCTTGAGAACTTGGACGGTAGCTTCCGTGTTCTGCCAAGTATCGAA 960
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QY 1141 CGTATCGTTGCTCACTAGTGTAGGGTGTCAAGAACTTGTCTTCACTTGTACGA 1200
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Db 1621 AGCACCTCAGAGTTAACATCACTGACCACTTTCTCAAGATATCGTTCAGGATTCGT 1680
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Db 1681 TAGCATCTACACATACTTGCAATTCACACCTCCATGACGGAAGGCTATCAATCAG 1740
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QY 1741 GGTAACTTCTCCGCAACATATGCAAGCGGAGCAACTTGGCAATCCGACGCTTCAGAAC 1800
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Db 2281 CATCAGGAAACAGTGTATCACTTACAGTGTGCAACCAACATTTATGCGCTTATGTCAG 2340
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QY 2341 GTTGGCTTCTTACTAATTAATACACAACCTTTTGTTAACAACATTTGGGCTATATGGTC 2400
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Db 2581 CATCCTTGCGCAACGATGATGTTCAAGATGATGAAACATTTAAATTTGTAATGTTG 2640
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Db 2641 GATTGGTGTATGATGTGAGGC 2661

RESULT 3
AAA88921
ID AAA88921 standard; DNA; 2436 BP.
XX AAA88921;
AC
XX
XX
DT 05-MAR-2001 (first entry)
XX
DE Nucleotide sequence of CryIA(b)-RTB3 fusion in pFASTBAC1.
DE
XX
XX CryIA(b); crystal protein; ricin toxin B; RTB3; lectin;
KW insecticide; pesticide; toxin; transgenic plant; insect resistance;
KW crop protection; pFASTBAC1; de.
XX
XX Chimeric - Bacillus thuringiensis.
OS Chimeric - Baculovirus.
OS Chimeric - Baculovirus.
XX
XX WO20006755-A2.
XX
XX 09-NOV-2000.
PD
XX
XX 27-APR-2000; 2000MO-GB01633.
PE
XX 28-APR-1999; 99GB-0009796.
PR
XX (PLAN-) PLANT BIOSCIENCE LTD.
PA
XX
XX Christou P, Mehio L;
PI
XX WPI; 2001-007228/01.
DR
XX
XX
PT Novel nucleic acid molecule encoding a pesticidal fusion polypeptide
PT comprising a toxin and a binding domain for producing transgenic plants
PT resistant to pests -
XX
XX
PS Claim 11; Fig 3h; 81pp; English.
XX
XX This nucleotide sequence is that of a fusion between DNA encoding
CC crystal protein CryIA(b) (see AAA88914) of Bacillus thuringiensis and
CC DNA encoding ricin toxin B RTB3 (see AAA88918) in baculovirus transfer
CC vector pFASTBAC1, in which the fusion was cloned under the control
CC of the polyhedrin promoter. This is an example of claimed nucleic
CC acids encoding pesticidal fusion proteins between a toxin domain
CC and a heterologous binding domain capable of binding non-specifically
CC to a cell membrane without disrupting that membrane. The use of such
CC fusions may help to inhibit the acquisition of resistance in a pest
CC population treated with the protein. Vectors (e.g. baculovirus
CC vectors or vectors suitable for use in a plant) host cells, and
CC transgenic plants (especially rice or maize) are also provided.

CC Expression of the fusion protein in a plant is useful for influencing
CC or affecting the toxicity of a plant to a pest, allowing control of
CC e.g. Lepidoptera, Coleoptera, Culicidae, Hymenoptera,
CC Homoptera, Diptera and Orthoptera pests.
XX
SO Sequence 2436 BP; 654 A; 617 C; 521 G; 644 T; 0 other;

Query Match 86.4%; Score 2407.6; DB 22; Length 2436;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 2416; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 AAATAGTATTTTACCTTTTTCGTAACAGTTTGTATTAATAAAACCTATTAATTCG 60
Db 1 AAATAGTATTTTACCTTTTTCGTAACAGTTTGTATTAATAAAACCTATTAATTCG 60
Qy 61 GATTATTCATACCGTCCACCATCGGCGCGGATGATGACAAACCAACATCAAC 120
Db 61 GATTATTCATACCGTCCACCATCGGCGCGGATGATGACAAACCAACATCAAC 120
Qy 121 GAATGATTCATACCACTGCTTGAGTAAACCCAGAACTGAAGTACTTGTGAGAAC 180
Db 121 GAATGATTCATACCACTGCTTGAGTAAACCCAGAACTGAAGTACTTGTGAGAAC 180
Qy 181 ATTGAACCGGTACACCTCCATGACATCTCTTCTTGACACAGTTTCTGACG 240
Db 181 ATTGAACCGGTACACCTCCATGACATCTCTTCTTGACACAGTTTCTGACG 240
Qy 241 GAGTTGTCGAGAGTGGTGGTGGTCTGCTGCGATGATGACATCATCTGGGGATCTTT 300
Db 241 GAGTTGTCGAGAGTGGTGGTGGTCTGCTGCGATGATGACATCATCTGGGGATCTTT 300
Qy 301 GGTCCATCTCAATGGAGATGATCTCTGTCGAAATTAAGACAGTTGATCAACAGATC 360
Db 301 GGTCCATCTCAATGGAGATGATCTCTGTCGAAATTAAGACAGTTGATCAACAGATC 360
Qy 361 GAAAGATTCGCGAGAAACCGGCGCATCTTAAGTTGAAAGATGAGCAATCTCAACAA 420
Db 361 GAAAGATTCGCGAGAAACCGGCGCATCTTAAGTTGAAAGATGAGCAATCTCAACAA 420
Qy 421 ATCTATGAGAGAGCTTCAGAGAGTGGAGCCGATCCTTAACCCAGCTCTCGCGAG 480
Db 421 ATCTATGAGAGAGCTTCAGAGAGTGGAGCCGATCCTTAACCCAGCTCTCGCGAG 480
Qy 481 GAAATGCGTATTCATTAATTCACGATGAAACGCGCTTGACACAGCTATCCATTTTC 540
Db 481 GAAATGCGTATTCATTAATTCACGATGAAACGCGCTTGACACAGCTATCCATTTTC 540
Qy 541 GCACTCCAGAACTACCAAGTCTCTCTGTCGCTGATGACGTTCAAGCAAGCTAATCTTAC 600
Db 541 GCACTCCAGAACTACCAAGTCTCTCTGTCGCTGATGACGTTCAAGCAAGCTAATCTTAC 600
Qy 601 CTCAGCGTCTTGAGAGAGTGAAGGTTGGGCAAAAGTGGGATTCGATGTCGAAC 660
Db 601 CTCAGCGTCTTGAGAGAGTGAAGGTTGGGCAAAAGTGGGATTCGATGTCGAAC 660
Qy 661 ATCAATAGCCGTTTCAACAGACCTTAAGCTGATGGAATCTACCGACGACGCTGTT 720
Db 661 ATCAATAGCCGTTTCAACAGACCTTAAGCTGATGGAATCTACCGACGACGCTGTT 720
Qy 721 CGTTGCTACACACGCTGCTGAGCGTGTGGGGTCTGATCTAGAGATTGATGA 780
Db 721 CGTTGCTACACACGCTGCTGAGCGTGTGGGGTCTGATCTAGAGATTGATGA 780
Qy 781 TACAACCAAGTTCAGAGAGAAATTCCTCAGATTTTGAATGATGATGATGA 840
Db 781 TACAACCAAGTTCAGAGAGAAATTCCTCAGATTTTGAATGATGATGATGA 840
Qy 841 AACTATGCTCCAGAACTTACCTTATCGCTACAGTGTCCCAATTAACAGAAATCTAT 900
Db 841 AACTATGCTCCAGAACTTACCTTATCGCTACAGTGTCCCAATTAACAGAAATCTAT 900
Qy 901 ACTAACCGAGTTCTTGAGAACTGCAAGGTAGCTTCGTTGCTGCAAGTATCGAA 960
Db 901 ACTAACCGAGTTCTTGAGAACTGCAAGGTAGCTTCGTTGCTGCAAGTATCGAA 960

D5	901	ACTAACCAGTCTTTGGAACCTTGACGAGTATCGTGGTCTCTGCCAAGGATCGAA	960
QY	961	GGCTTCATCGAGAGCCCACTTGATGACATCTTGAACAGCATATCTACACCGAT	1020
D5	961	GGCTTCATCGAGAGCCCACTTGATGAGACATCTTGAACAGCATATCTACACCGAT	1020
QY	1021	GCTCAAGAGGAGATTAACCTGGTCTGGGACACAGATCAATGGCTCTCCAGTTGATTC	1080
D5	1021	GCTCAAGAGGAGATTAACCTGGTCTGGGACACAGATCAATGGCTCTCCAGTTGATTC	1080
QY	1081	AGCGGGCCGAGTTTACCTTCTCTGTATGGAATAATGGGAAAGCGCGTCCACAACAA	1140
D5	1081	AGCGGGCCGAGTTTACCTTCTCTGTATGGAATAATGGGAAAGCGCGTCCACAACAA	1140
QY	1141	CGTATCGTGTCTCACTAAGTGCAGGGGTCTACAGAACCTTGTCTTCCACTTGTACAGA	1200
D5	1141	CGTATCGTGTCTCACTAAGTGCAGGGGTCTACAGAACCTTGTCTTCCACTTGTACAGA	1200
QY	1201	AGACCCCTTCAATTCGGATTCGAACAACACAGAACCTTCCGTTCTTGACGGAAAGATTC	1260
D5	1201	AGACCCCTTCAATTCGGATTCGAACAACACAGAACCTTCCGTTCTTGACGGAAAGATTC	1260
QY	1261	GCCTATGGAACCTCTTCTTAACCTTGCCATCCGCTTTTACAGAAAGACGGAAACCGTTGAT	1320
D5	1261	GCCTATGGAACCTCTTCTTAACCTTGCCATCCGCTTTTACAGAAAGACGGAAACCGTTGAT	1320
QY	1321	TCCTTTGACGAATATCCACACAGAACCAACATGTGCCACCGACGACAGATTTCTCCAC	1380
D5	1321	TCCTTTGACGAATATCCACACAGAACCAACATGTGCCACCGACGACAGATTTCTCCAC	1380
QY	1381	AGGTTGAGCCACGTTGCATGTTCCGTTCCGGATTTACAGAACATGTTCCGTGAGATCATC	1440
D5	1381	AGGTTGAGCCACGTTGCATGTTCCGTTCCGGATTTACAGAACATGTTCCGTGAGATCATC	1440
QY	1441	AGAGCTCCTAATGTTCTCAATGATTCATGATGTGATGATTCGAACAATATCATCTTCTCC	1500
D5	1441	AGAGCTCCTAATGTTCTCAATGATTCATGATGTGATGATTCGAACAATATCATCTTCTCC	1500
QY	1501	TCTCAATACACCCAAATCCCAATGACCAAGTCTACTAACTTGGATCTGGAACCTTCTGC	1560
D5	1501	TCTCAATACACCCAAATCCCAATGACCAAGTCTACTAACTTGGATCTGGAACCTTCTGC	1560
QY	1561	GTGAAGAAGACCAAGCTTCAACAGAGGTATTTCTTAAAGAACCTTCTCCGCGCAGATT	1620
D5	1561	GTGAAGAAGACCAAGCTTCAACAGAGGTATTTCTTAAAGAACCTTCTCCGCGCAGATT	1620
QY	1621	AGCACCCCTCAGAGTTAATCATCATGCGACACATTTCTCAAAATATTCGTGAGGATTCGT	1680
D5	1621	AGCACCCCTCAGAGTTAATCATCATGCGACACATTTCTCAAAATATTCGTGAGGATTCGT	1680
QY	1681	TACGCATCTACCACTTAATCTTGACACTTCACACTTCGATCGACGGAAGGCTTATCAATCAG	1740
D5	1681	TACGCATCTACCACTTAATCTTGACACTTCACACTTCGATCGACGGAAGGCTTATCAATCAG	1740
QY	1741	GGTAACTTCTCGCAACCATGTCAAGCGGACAGCACTTGCAATCCGCGACCTTCAGAAC	1800
D5	1741	GGTAACTTCTCGCAACCATGTCAAGCGGACAGCACTTGCAATCCGCGACCTTCAGAAC	1800
QY	1801	GTCGGTTTCACTACCTTTCAACTTCTCTAAGGATCAAGCGTTTCAACCTTAAGCGCT	1860
D5	1801	GTCGGTTTCACTACCTTTCAACTTCTCTAAGGATCAAGCGTTTCAACCTTAAGCGCT	1860
QY	1861	CATGTGTTCAATTCTGGCAATGAATGTACATTGACCGTATTTGATTTGTGCTGCCGAA	1920
D5	1861	CATGTGTTCAATTCTGGCAATGAATGTACATTGACCGTATTTGATTTGTGCTGCCGAA	1920
QY	1921	GTTACCTTTCGAGGCTGAGTACTGAGAAATTCATGCTGATGTTTGTATGATCTCGAGCCCA	1980
D5	1921	GTTACCTTTCGAGGCTGAGTACTGAGAAATTCATGCTGATGTTTGTATGATCTCGAGCCCA	1980
QY	1981	TAGTGCATTCGTAAGTTCGAAATTTGATGATGTTGATGTTAAGGATGGAAGATTCACCA	2040
D5	1981	TAGTGCATTCGTAAGTTCGAAATTTGATGATGTTGATGTTAAGGATGGAAGATTCACCA	2040

Oy	2041	ACGGAAACGAATPACAGTGTGGCGCATGCAAGTCTATATACAGATGCAAAATCAGCTCTGGA	2100
Db	2041	ACGGAAACGAATPACAGTGTGGCGCATGCAAGTCTATATACAGATGCAAAATCAGCTCTGGA	2100
Oy	2101	CTTTGAAAGAGCAATACTATTGCAATCTAATGAAAGTGTTAATCTTAACCTTACGGGTACA	2160
Db	2101	CTTTGAAAGAGCAATACTATTGCAATCTAATGAAAGTGTTAATCTTAACGGGTACA	2160
Oy	2161	GTCGGGAGTCTATATGTATGATCTATATATTTGCAATACTGCTGCAACTGATGCCACCCGCT	2220
Db	2161	GTCGGGAGTCTATATGTATGATCTATATATTTGCAATACTGCTGCAACTGATGCCACCCGCT	2220
Oy	2221	GGCAATATGGAATATGAAACCATCATATAATCCCAAGTCTAGTCTAGTTTATGACAGCA	2280
Db	2221	GGCAATATGGAATATGAAACCATCATATAATCCCAAGTCTAGTCTAGTTTATGACAGCA	2280
Oy	2281	CATCAGGGAACAGTGTGATCCACACTTACCGGTGCAACCAATTTATGCCGTTATGTCAG	2340
Db	2281	CATCAGGGAACAGTGTGATCCACACTTACCGGTGCAACCAATTTATGCCGTTATGTCAG	2340
Oy	2341	GTTGGCTTCCATCAATATATPACAACTTTGTTACAAACATGTTGGGCTATATGCTC	2400
Db	2341	GTTGGCTTCCATCAATATATPACAACTTTGTTACAAACATGTTGGGCTATATGCTC	2400
Oy	2401	TGTGCTTGCAAGCAATATAGTGCACAAGT 2430	
Db	2401	TAACTTGTGCAAGACTATGAGAGTCAAT 2430	
RESULT 4			
ID	AAA88922	standard; DNA; 2788 BP.	
AC	AAA88922;		
XX			
DT	05-MAR-2001	(first entry)	
XX			
DE	Nucleotide sequence of CryIA(c)-RTB1 fusion in pFASTBAC1.		
XX			
KM	CryIA(c); crystal protein; ricin toxin B; RTB1, lectin;		
KM	insecticide; pesticide; toxin; transgenic plant; insect resistance;		
KM	crop protection; pFASTBAC1; de.		
XX			
OS	Chimeric - Bacillus thuringiensis.		
OS	Chimeric - Ricinus communis.		
OS	Chimeric - Baculovirus.		
XX			
PN	WO20006755-A2.		
XX			
PD	09-NOV-2000.		
XX			
PF	27-APR-2000; 2000WO-GB01633.		
PR	28-APR-1999; 99GB-0009796.		
XX			
PA	(PLAN-) PLANT BIOSCIENCE LTD.		
XX			
PI	Christou P, Mehlo L;		
XX			
DR	WPI; 2001-007228/01.		
PT			
PT	Novel nucleic acid molecule encoding a pesticidal fusion polypeptide		
PT	comprising a toxin and a binding domain for producing transgenic plants		
PT	resistant to pests -		
XX			
PS	Claim 11; Fig 3i; 81pp; English.		
XX			
CC	This nucleotide sequence is that of a fusion between DNA encoding		
CC	crystal protein CryIA(c) (see AAA88915) of Bacillus thuringiensis and		
CC	DNA encoding ricin toxin B RTB1 (see AAA88916) in baculovirus transfer		
CC	vector pFASTBAC1, in which the fusion was cloned under the control		
CC	of the polyhedrin promoter. This is an example of claimed nucleic		

QY	1915	GCCGAGATTACCTTCGAGGCGTAGTACTGAAATTCATTCGCGATGTTTGTATGGAATCCTG	1974
Db	1918	GTACTGCGAACACTCTCGAGGCTG---AATGAAATTCATGCTGAGTGTGTGATGGAATCCTG	1974
QY	1975	AGCCCATATGATCGCATCGTAGTGGAAATGCTCATATGATGTTAGTATAGGATGGAAGAT	2034
Db	1975	AGCCCATATGATCGCATCGTAGTGGAAATGCTCATATGATGTTAGTATAGGATGGAAGAT	2034
QY	2035	TCGACAAACGGAACCGCAATACAGTTGTGGCCATGSCAAGTCTTAATACAGATGCAATAGC	2094
Db	2035	TCGACAAACGGAACCGCAATACAGTTGTGGCCATGSCAAGTCTTAATACAGATGCAATAGC	2094
QY	2095	TCTGGACTTTTAAAAAGAGACAACTACTTATGATCTTAATGGAAGTGTTTAACTACTACG	2154
Db	2095	TCTGGACTTTTAAAAAGAGACAACTACTTATGATCTTAATGGAAGTGTTTAACTACTACG	2154
QY	2155	GGTACAGTCGGGAGTCTATATGTGATCTATATGCAATTCGCAATACGCTGCAACTGATGCA	2214
Db	2155	GGTACAGTCGGGAGTCTATATGTGATCTATATGCAATTCGCAATACGCTGCAACTGATGCA	2214
QY	2215	CCCGCTGGCAATATGAGGATATGGAACCAATCATTAATCCGAGATCTAGTCTAGTTTATG	2274
Db	2215	CCCGCTGGCAATATGAGGATATGGAACCAATCATTAATCCGAGATCTAGTCTAGTTTATG	2274
QY	2275	CAGGACATCAAGGGAACAGTGTGACACACTTACGGTGCAAAACCAACTTTATCCGTTA	2334
Db	2275	CAGGACATCAAGGGAACAGTGTGACACACTTACGGTGCAAAACCAACTTTATCCGTTA	2334
QY	2335	GTCAAGGTGGCTTCCTACTAATATATACAGAACCTTTGTTACAAACCTTGTGGGCTAT	2394
Db	2335	GTCAAGGTGGCTTCCTACTAATATATATACAGAACCTTTGTTACAAACCTTGTGGGCTAT	2394
QY	2395	ATGGTCTGTGCTTGCAACAAATATGTGACAAATATGGAATGGAATGGAAGCATGTAGCATGAA	2454
Db	2395	ATGGTCTGTGCTTGCAACAAATATGTGACAAATATGGAATGGAATGGAAGCATGTAGCATGAA	2454
QY	2455	AGGCTGAAACAACAGTGGGCTCTTTATGCAATGTTCAATACGCTCTCAGCAAAACCGAG	2514
Db	2455	AGGCTGAAACAACAGTGGGCTCTTTATGCAATGTTCAATACGCTCTCAGCAAAACCGAG	2514
QY	2515	ATAATTTGCTTACAAGATATCTAATATACGGGAAACAGTGTATGAATTCCTCTCTGTG	2574
Db	2515	ATAATTTGCTTACAAGATATCTAATATACGGGAAACAGTGTATGAATTCCTCTCTGTG	2574
QY	2575	GGCCGTGACCTCTGCGCAACGATGGATGTTCAAGAAAGATGGAACCAATTTTAAATTTGT	2634
Db	2575	GGCCGTGACCTCTGCGCAACGATGGATGTTCAAGAAAGATGGAACCAATTTTAAATTTGT	2634
QY	2635	ATAGTGAATTTGATTTAGATGTGAGCGCATCGGATCCGAGCCTTAAACAAATCAATCTTT	2694
Db	2635	ATAGTGAATTTGATTTAGATGTGAGCGCATCGGATCCGAGCCTTAAACAAATCAATCTTT	2694
QY	2695	ACCCTCTTCATGATGACCCCAAAACCAAAATATGTTATCCATTTATTTGATGACAGATTACA	2754
Db	2695	ACCCTCTTCATGATGACCCCAAAACCAAAATATGTTATCCATTTATTTGATGACAGATTACA	2754
QY	2755	AGCTTGTCGAGAACTAGAGATCATTAATCAG	2788
Db	2755	AGCTTGTCGAGAACTAGAGATCATTAATCAG	2788
RESULT 5			
AAA88923			
ID	AAA88923 standard; DNA; 2692 BP.		
XX	AAA88923;		
XX	05-MAR-2001 (first entry)		
DE	Nucleotide sequence of CryIa(c)-RTB2 fusion in pFASTBAC1.		
XX	CryIa(c); crystal protein; ricin toxin B; RTB2; lectin;		
KM	insecticide; pesticide; toxin; transgenic plant; insect resistance;		

KM	crop protection; pFASTBAC1; ds.
XX	Chimeric - Bacillus thuringiensis.
OS	Chimeric - Ricinus communis.
OS	Chimeric - Baculovirus.
PX	W020006755-A2.
XX	
XX	09-NOV-2000.
PD	
XX	27-APR-2000; 2000WO-G801633.
PF	
XX	28-APR-1999; 99GB-0009796.
FR	(PLAN-) PLANT BIOSCIENCE LTD.
XX	
XX	Christou P, Mehlo L;
PI	
XX	WPI; 2001-007228/01.
DR	
XX	
PT	Novel nucleic acid molecule encoding a pesticidal fusion polypeptide
PT	comprising a toxin and a binding domain for producing transgenic plants
PT	resistant to pests
PS	-
XX	
XX	Claim 11; Fig 3j; 81pp; English.
CC	This nucleotide sequence is that of a fusion between DNA encoding
CC	crystal protein CryIA(c) (see AAA88915) of Bacillus thuringiensis and
CC	DNA encoding ricin toxin B RTB2 (see AAA88917) in baculovirus transfer
CC	vector pRASTBAC1, in which the fusion was cloned under the control
CC	of the polyhedrin promoter. This is an example of claimed nucleic
CC	acids encoding pesticidal fusion proteins between a toxin domain
CC	and a heterologous binding domain capable of binding non-specifically
CC	to a cell membrane without disrupting that membrane. The use of such
CC	fusions may help to inhibit the acquisition of resistance in a pest
CC	population treated with the protein. Vectors (e.g. baculovirus
CC	vectors or vectors suitable for use in a plant), host cells, and
CC	transgenic plants (especially rice or maize) are also provided.
CC	Expression of the fusion protein in a plant is useful for influencing
CC	or affecting the toxicity of a plant to a pest, allowing control of
CC	e.g. Lepidoptera, Coleoptera, Culicidae, Simuliidae, Hymenoptera,
CC	Homoptera, Diptera and Orthoptera pests.
XX	
SQ	Sequence 2692 BP; 736 A; 640 C; 592 G; 724 T; 0 other;
<hr/>	
Query March	79.1%; Score 2204.6; DB 22; Length 2692;
Best Local Similarity	90.2%; Pred. No. 0;
Matches 2406; Conservative	0; Mismatches 249; Indels 12; Gaps 4;
OY	1 AAATAGATTATTTACTGTTTTCTGTACAGTTTGTAAATAAAAAACCATTAAATTCCG 60
DB	1 AAATAGATTATTTACTGTTTTCTGTACAGTTTGTAAATAAAAAACCATTAAATTCCG 60
OY	61 GATTATTCATRCGGTCCCAACCATGCGGCGCGGATCCATGACAACAACCCAAACATCAAC 120
DB	61 GATTATTCATRCGGTCCCAACCATGCGGCGCGGATCCATGACAACAACCCAAACATCAAC 120
OY	121 GAATGCATTCATCAACAACCTGGTTAGTAGTAACCCAGAAGTTGAAGTACTTGTTGGAGAACGC 180
DB	121 GAATGCATTCATCAACAACCTGGTTAGTAGTAACCCAGAAGTTGAAGTACTTGTTGGAGAACGC 180
OY	181 ATTGAAAACCGGTACACTGCCCATCGACATCTCCTTGTCCTTGAGACAGATTTCTGCTACG 240
DB	181 ATTGAAAACCGGTACACTGCCCATCGACATCTCCTTGTCCTTGAGACAGATTTCTGCTACG 240
OY	241 GAGTTCGTCGACAGTGTGGGTGTTCTTCGGAAGTATGATCATCATCTGGGGATATCTTT 300
DB	241 GAGTTCGTCGACAGTGTGGGTGTTCTTCGGAAGTATGATCATCATCTGGGGATATCTTT 300
OY	301 GGTCATTCATCAATGGAGATGATTCCTGGTGCAGAAATTGACAGTTGATCAACAGAGATC 360
DB	301 GGTCATTCATCAATGGAGATGATTCCTGGTGCAGAAATTGACAGTTGATCAACAGAGATC 360

QY	361	GAAGAGTTTCCGACGAAACCAAGGCCATCTCTAGTTGGAGATTGAGCAATCTCTACCA	420
Db	361	GAAGAGTTTCCGACGAAACCAAGGCCATCTCTAGTTGGAGATTGAGCAATCTCTACCA	420
QY	421	ATCTATCGAGAGACTTCAGAGACTGGGAAAGCCGATCCTCTAATCCAGCTCTCCGAG	480
Db	421	ATCTATCGAGAGACTTCAGAGACTGGGAAAGCCGATCCTCTAATCCAGCTCTCCGAG	480
QY	481	GAATGCGTATCAATTCAACGACATGAACCGCTTGAACAAGCTATCCATTGTTTC	540
Db	481	GAATGCGTATCAATTCAACGACATGAACCGCTTGAACAAGCTATCCATTGTTTC	540
QY	541	GCAGTCCAGAACTACCAAGTCTCTCTGTCGTACGTTCAAGACGTAATCTTTCAC	600
Db	541	GCAGTCCAGAACTACCAAGTCTCTCTGTCGTACGTTCAAGACGTAATCTTTCAC	600
QY	601	CTCAGCGGCTTCGAGACGTTAGGGTGTTGGGCAAGTGGGGATTCGATGCTGCAAC	660
Db	601	CTCAGCGGCTTCGAGACGTTAGGGTGTTGGGCAAGTGGGGATTCGATGCTGCAAC	660
QY	661	ATCATATAGCCCTTACCAAGACCTTACTAGGCTGATTGGAAACTACACCGACCAAGCTGTT	720
Db	661	ATCATATAGCCCTTACCAAGACCTTACTAGGCTGATTGGAAACTACACCGACCGTGT	720
QY	721	CGTTGGTACAAACACTGCGTTGGAGCGTGTCGSGGCTCTGATTTCTAGAGATTGATAGA	780
Db	721	CGTTGGTACAAACACTGCGTTGGAGCGTGTCGSGGCTCTGATTTCTAGAGATTGATAGA	780
QY	781	TACAAACGATTACAGAGAGAAATTGACCCCTCAAGTTTGGACATTTGTCCTCTCCG	840
Db	781	TACAAACGATTACAGAGAGAAATTGACCCCTCAAGTTTGGACATTTGTCCTCTCCG	840
QY	841	AACTATGACTCCAGAACCTTACCCTATCCGTACAGTGTCCCACTTACAGAGAAATCTAT	900
Db	841	AACTATGACTCCAGAACCTTACCCTATCCGTACAGTGTCCCACTTACAGAGAAATCTAT	900
QY	901	ACTAACCCAGTTCCTTGAGAACTTGAACGGTACCTTCGGTGTCTGCCAAGTATCGAA	960
Db	901	ACTAACCCAGTTCCTTGAGAACTTGAACGGTACCTTCGGTGTCTGCCAAGTATCGAA	960
QY	961	GGCTTCATCAGAGAGCCCACTTGTATGACATCTTGAAACAGCATATATCTAACCCGAT	1020
Db	961	GGCTTCATCAGAGAGCCCACTTGTATGACATCTTGAAACAGCATATATCTAACCCGAT	1020
QY	1021	GCTACAGAGAGAGTATTACTGCGCTGAGAACCAAGCATAGGGCTCTCCAGTTGGAATTC	1080
Db	1021	GCTACAGAGAGAGTATTACTGCGCTGAGAACCAAGCATAGGGCTCTCCAGTTGGAATTC	1080
QY	1081	AGCGGGCCGAGTTTACCTTTCCTCTCTATGGAATATGAGAAACGCCGCTCCACAACAA	1140
Db	1081	AGCGGGCCGAGTTTACCTTTCCTCTCTATGGAATATGAGAAACGCCGCTCCACAACAA	1140
QY	1141	CGTATCGTTTGCTCAACTAGGTCAAGGATGCTACAGAACCTTGTCTTCCACTTGTACAGA	1200
Db	1141	CGTATCGTTTGCTCAACTAGGTCAAGGATGCTACAGAACCTTGTCTTCCACTTGTACAGA	1200
QY	1201	AGACCCCTCAATATGATATCAACAACACAGCAAACTTTCGTTCTTGAACGAAACAGATTC	1260
Db	1201	AGACCCCTCAATATGATATCAACAACACAGCAAACTTTCGTTCTTGAACGAAACAGATTC	1260
QY	1261	GCTATGGAACCTCTTCTTCACTTGGCATCGCTGTTTACAGAAAGCGGAAACGGTTGAT	1320
Db	1261	GCTATGGAACCTCTTCTTCACTTGGCATCGCTGTTTACAGAAAGCGGAAACGGTTGAT	1320
QY	1321	TCCTTGGACGAAATCCACACAGAAACAATGTGCCACCGGCAAGATTTCTCCAC	1380
Db	1321	TCCTTGGACGAAATCCACACAGAAACAATGTGCCACCGGCAAGATTTCTCCAC	1380
QY	1381	AGGTGAGACAGTGTCAATGTTCCGTTCCGGATTCACCAACAGTTCGCTGAGCATCATC	1440
Db	1381	AGGTGAGACAGTGTCAATGTTCCGTTCCGGATTCACCAACAGTTCGCTGAGCATCATC	1440
QY	1441	AGAGTCCCATGTTCTCATGATTCATCGTATGCTGAGTTCAACATATCATTTCTTCC	1500

Db	1441	AGAGCTCTTATGTTCTTGGATACACCGTAGTCTAGTTCAACAAACATCATCGCATCC	1500
Oy	1501	TCCTCAATATCACCCAAATCCCAATTGACCAAGCTCTACTAACTTGGATCTGCAACTTCTGTC	1560
Db	1501	GATAGTATTAATCAAAATCCCTCGAGGTGAAG---GGAACTTTCTCTTCAACGGTTCTGTCT	1557
Oy	1561	GTCGAAGACCAAGGCTTTCACAGAGGTATATTTCTTGAAGAACTTCTCTCGCCAGATT	1620
Db	1558	ATTTTCAGAGACAGAGATTCACTGGTGGAGACCTCGTTAGACTCAACACAGTGGAAATAC	1617
Oy	1621	AGCACCTCTAGAGTTAACTATCATCGACCACTT---TCTGAAGATATTCGTGCAGATT	1677
Db	1618	ATTTCAGAAATGAGGGTATATTGAAGTTCCAAATTACTTCCATCCACATCTTACCAAGATAT	1677
Oy	1678	CGTTACCCATCTTACACCTAACTTGGCAATTCGCACACCTCCATCGACGGAAGGCTTATCAAT	1737
Db	1678	AGATTTGCTGTGAGAGTATGCTTCTGTGACCCCTTATCACCCTCAACGTTAATTTGGGGTAT	1737
Oy	1738	CAGGGTAACTTCTCCGCAACCATGTCA---AGCGGACGAACTTGGCAATCCGGACGCTTC	1794
Db	1738	TCATCCATCTTCTCCAAATACAGTTCCAGCTACAGCTACCTCTTGGATATCTCCAAATCC	1797
Oy	1795	AGAACCGTCCGTTTCACTACTCCCTTTCGAACCTTCTCTAAGGATCAAGGCTTTCACCTT	1854
Db	1798	AGCGATTTCCGTTACTTTGAAAGGCCAAAGCTTTTACATCTTCACTCGGTAACATCGTG	1857
Oy	1855	AGCGCTCATGTGTTCAATTCGTGGCAATGAAGTGTACATTCGACCGTATTTGAGTTGTGCT	1914
Db	1858	GGTTTGAAGAACTTTAGTGGGACCTGACAGAGTATTTTCACACAAATTCGAGTTCAATTC	1917
Oy	1915	GCCGAAGTTACTTCGAGGCTGAGTACTGAGAAATTCATGCTGATGTTTGTATGGATCCTG	1974
Db	1918	GTTACTGCAACACTCGAGGCTG---AATGAGAAATTCATGCTGATGTTTGTATGGATCCTG	1974
Oy	1975	AGCCCATATGTCGTATCGTAGTGGAAATGGTCTATGTGTGATGTTAAGGATGGAAAT	2034
Db	1975	AGCCCATATGTCGTATCGTAGTGGAAATGGTCTATGTGTGATGTTAAGGATGGAAAT	2034
Oy	2035	TCCAACACGGAAACGCAATACAGTTGTGGCCANTGCAAGTCTAATACAGATSCAAATCAGC	2094
Db	2035	TCCAACACGGAAACGCAATACAGTTGTGGCCANTGCAAGTCTAATACAGATSCAAATCAGC	2094
Oy	2095	TCTGGACTTTGAAAAGAGACAATATCTATTCGATCTAATGGAAGTGTTTAACTACTTACG	2154
Db	2095	TCTGGACTTTGAAAAGAGACAATATCTATTCGATCTAATGGAAGTGTTTAACTACTTACG	2154
Oy	2155	GGTACAGTCCGGAGCTATATGTATGATCTATATGATTGCATAATCTCTGCCAATGATGCCA	2214
Db	2155	GGTACAGTCCGGAGCTATATGTATGATCTATATGATTGCATAATCTCTGCCAATGATGCCA	2214
Oy	2215	CCCGCTGGCAAAATATGGGATATATGGAACCAATCATTAATCCAGATCTAGTCTAGTTTACG	2274
Db	2215	CCCGCTGGCAAAATATGGGATATATGGAACCAATCATTAATCCAGATCTAGTCTAGTTTACG	2274
Oy	2275	CAGCGACATCAGGGAACAGTGTGATCCACACTTACGGTGCAAACCAACATTTATGTCGGTTA	2334
Db	2275	CAGCGACATCAGGGAACAGTGTGATCCACACTTACGGTGCAAACCAACATTTATGTCGGTTA	2334
Oy	2335	GTCGAAGTTGGCTTCTCTAATATATACAACTTTTGTATACAACTTGTGGGCTAT	2394
Db	2335	GTCGAAGTTGGCTTCTCTAATATATACAACTTTTGTATACAACTTGTGGGCTAT	2394
Oy	2395	ATGCTCTGTGCTTGCAGCAAAATAGTGACAAAGTATGAGATAGAGGACTGTAGCACTGAAA	2454
Db	2395	ATGCTCTGTGCTTGCAGCAAAATAGTGACAAAGTATGAGATAGAGGACTGTAGCACTGAAA	2454
Oy	2455	AGGCTGAAACAACAGTGGGCTCTTTATATGACAGATGGTTCAATACGTCCTCAGCAAAACGAG	2514
Db	2455	AGGCTGAAACAACAGTGGGCTCTTTATATGACAGATGGTTCAATACGTCCTCAGCAAAACGAG	2514
Oy	2515	ATAATTGCTTACAGTATTTCTAATATACGGGAAACAGTTGTTAAGTCTCTCTTGTG	2574
Db	2515	ATAATTGCTTACAGTATTTCTAATATACGGGAAACAGTTGTTAAGTCTCTCTTGTG	2574

Db 1081 AGCGGCCCGAGTTTACCTTCTCTCTATGGAACATAGGAAAGCCCGCTCCACAACA 1140
 Qy 1141 CGTATCGTTGCTCACTAGGTGAGGGTGTCTACAGAACTTGTCTTCCACTTTAGAGA 1200
 Db 1141 CGTATCGTTGCTCACTAGGTGAGGGTGTCTACAGAACTTGTCTTCCACTTTAGAGA 1200
 Qy 1201 AGACCTTTCATATCGGTATCAACACAGCACTTTCCTGTTTGAACGAGATTG 1260
 Db 1201 AGACCTTTCATATCGGTATCAACACAGCACTTTCCTGTTTGAACGAGATTG 1260
 Qy 1261 GCCATAGGAACCTTTTCTAATTGCGCATCCGCTTTTACAGAAAGCGGAAACCGTTGAT 1320
 Db 1261 GCCATAGGAACCTTTTCTAATTGCGCATCCGCTTTTACAGAAAGCGGAAACCGTTGAT 1320
 Qy 1321 TCCCTTGACGAAATCCACACAGAAACAATGCGACCCGAGCAAGATTCTCCAC 1380
 Db 1321 TCCCTTGACGAAATCCACACAGAAACAATGCGACCCGAGCAAGATTCTCCAC 1380
 Qy 1381 AGGTTGAGCCACGTGTCCATGTTCCGTTCCGGAATTGACAAACAGTTCGTGAGCATATC 1440
 Db 1381 AGGTTGAGCCACGTGTCCATGTTCCGTTCCGGAATTGACAAACAGTTCGTGAGCATATC 1440
 Qy 1441 AGACCTTCTATGTTCTCATGATTCATGTAGTGTGATGCAACAATATGATTCCTTCC 1500
 Db 1441 AGACCTTCTATGTTCTCATGATTCATGTAGTGTGATGCAACAATATGATTCCTTCC 1500
 Qy 1501 TCTCAATATCAACCAATCCCAATTCAGCAAGTCTACTAACTTTGATCTGAACTTCTGTC 1560
 Db 1501 GATAGTATTAATCTCAAAATCCCTGCAAGTAGAAGGA---AACTTCTCTTCAACGGTTCTGTC 1557
 Qy 1561 GTGAAGGACACGAGCTTCAACAGAGGTATATCTTAGAAGAACTTCTCTGCGCAGATT 1620
 Db 1558 ATTTCAAGGACACGAGCTTCAACAGAGGTATATCTTAGAAGAACTTCTCTGCGCAGATT 1617
 Qy 1621 AGACCTCTCAGAGTTAATCATCATCTGACACCACTT---TCTCAAGATATCGGTGAGATT 1677
 Db 1618 ATTCAGAATAGAGGATATATGAAAGTTCAATTCATCTCCATCCACATCTACAGATAT 1677
 Qy 1678 CGTTACGATCTACCACTAACCTTCGAAATTCACACCTTCATGACGGAAGGCTATCAAT 1737
 Db 1678 AGACTGTGTGAGGATATGCTTCTGTGACCCCTATATCCCTCAACGTTAATTTGGGTAT 1737
 Qy 1738 CAGGGTAACTTCTCCGCAACCATGTCA---AGCGGACGAACTTGCAATCCGGAGCTTC 1794
 Db 1738 TCATTCATCTTCTCCAAATACAGTTCCAGCTACAGCTACCTCTTGGAATATCTCCAAATCC 1797
 Qy 1795 AGAACCGTCCGTTTCACTACTCTTTCGAACTTCTTAACGGAATCAAGGTTTCACTT 1854
 Db 1798 AGCATTTCCGGTACTTTGAAAGTCCAAATGCTTTTACATCTTCACTGGTAAACATCTGT 1857
 Qy 1855 AGCGCTCATGTTCATATTTCTGGCAATGAGTATGACCGTATGAGTTTGTGCT 1914
 Db 1858 GGTGTGAAACTTTAGTGGGACGTCGAGAGTATATGACAGATTGGAATCTTCA 1917
 Qy 1915 GCCCAAGTTACTTCGAGGCTGAGTACTGAGAAATTCATGCTGATGTTTGAATGATCTGT 1974
 Db 1918 GTTACTGCAACACTCTGAGGCTG---AATGAAATTCATGCTGATGTTTGAATGATCTGT 1974
 Qy 1975 AGCCCATATGTCGTATCGTAGTGAATGTCATATGTTGATGTTTGGATGGAAT 2034
 Db 1975 AGCCCATATGTCGTATCGTAGTGAATGTCATATGTTGATGTTTGGATGGAAT 2034
 Qy 2035 TCCCAACGGAACGCAATATAGTTGTGCGCATGCAAGTCTTAATACAGATGCAATACG 2094
 Db 2035 TCCCAACGGAACGCAATATAGTTGTGCGCATGCAAGTCTTAATACAGATGCAATACG 2094
 Qy 2095 TCTGGAATTTGAAAAGAGACAATATCTTCAATGAAAGTGTTTAACTACTTACG 2154
 Db 2095 TCTGGAATTTGAAAAGAGACAATATCTTCAATGAAAGTGTTTAACTACTTACG 2154
 Qy 2155 GGTACAGTCCGGGAGTCTATGATGATCTATGATGGAATATCTGCTGCAACTGATGCA 2214
 Db 2155 GGTACAGTCCGGGAGTCTATGATGATCTATGATGGAATATCTGCTGCAACTGATGCA 2214

Qy 2215 CCCGCTGGCAAAATATGGGATTAATGGAACCATATGAAATCCAGATCTAGTCTAGTTTAA 2274
 Db 2215 CCCGCTGGCAAAATATGGGATTAATGGAACCATATGAAATCCAGATCTAGTCTAGTTTAA 2274
 Qy 2275 CAGGACATCAAGGAACAGTGTACCACTTAAAGGTGCAAAACCAATTTATCCCTTA 2334
 Db 2275 CAGGACATCAAGGAACAGTGTACCACTTAAAGGTGCAAAACCAATTTATCCCTTA 2334
 Qy 2335 GTCAAGGTGGCTTCTTACTAATATATACAACTTTTGTATCAACCATTTGTTGGCTAT 2394
 Db 2335 GTCAAGGTGGCTTCTTACTAATATATACAACTTTTGTATCAACCATTTGTTGGCTAT 2394
 Qy 2395 ATGCTGTGCTTGCAGAACCAATATGAGACAGTAT 2430
 Db 2395 ATGCTGTGCTTGCAGAACCAATATGAGACAGTAT 2430

RESULT 7
 ID AAA88914
 AAA88914 standard; DNA; 2062 BP.
 XX
 AC AAA88914;
 XX
 DT 05-MAR-2001 (first entry)
 XX
 DE Nucleotide sequence of CryIA(b) in pFASTBAC1.
 XX
 KW CryIA(b); crystal protein; insecticide; pesticide; toxin;
 KW transgenic plant; insect resistance; crop protection; pFASTBAC1;
 KW ds.
 XX
 OS Chimeric - Bacillus thuringiensis.
 OS Chimeric - Baculovirus.
 XX
 EH Key Location/Qualifiers
 FT CDS 97..1944
 FT /*tag= a

MO20006755-A2.
 XX
 PN 09-NOV-2000.
 XX
 PD 27-APR-2000; 2000WO-GB01633.
 XX
 PE 28-APR-1999; 99GB-0009796.
 XX
 PR (PLAN-) PLANT BIOSCIENCE LTD.
 XX
 PA Christou P, Mehlo L;
 PI
 PI WPI: 2001-007228/01.
 DR
 XX
 XX Novel nucleic acid molecule encoding a pesticidal fusion polypeptide
 PT comprising a toxin and a binding domain for producing transgenic plants
 PT resistant to pests -
 XX
 XX
 PS Claim 9; Fig 3a; 81pp; English.

The present sequence is that of Bacillus thuringiensis crystal protein CryIA(b) DNA in baculovirus transfer vector pFASTBAC1, in which the gene was cloned under the control of the polyhedrin promoter. The invention provides nucleic acids (see AAA88919-24) encoding pesticidal fusion proteins comprising a toxin domain and a heterologous binding domain capable of binding non-specifically to a cell membrane without disrupting that membrane. The toxin domain is preferably obtained from CryIA(b) or CryIA(c), and the binding domain is preferably derived from a lectin, such as ricin toxin B chain. The use of such fusions may help to inhibit the acquisition of resistance in a pest population treated with the protein. Vectors (e.g. baculovirus vectors or vectors suitable for use in a plant), host cells, and transgenic plants (especially rice or maize) are also provided. Expression of the fusion protein in a

CC plant is useful for influencing or affecting the toxicity of a
CC plant to a pest, allowing control of e.g. Lepidoptera, Coleoptera,
CC Culiidae, Simuliidae, Hymenoptera, Homoptera, Diptera and
CC Orthoptera pests.

XX Sequence 2062 BP; 538 A; 552 C; 440 G; 532 T; 0 other;

Query Match 70.0%; Score 1951; DB 22; Length 2062;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1951; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 AATAAGATTATTAAGTCTTTTCTGTAACAGTTTGTATATAAAAAAAGCTATATATTCG 60
DB 1 AATAAGATTATTAAGTCTTTTCTGTAACAGTTTGTATATAAAAAAAGCTATATATTCG 60
QY 61 GATTATTCATACCGTCCACCATCGGGGGGGGATTCATGACAAACCCAAATCATAC 120
DB 61 GATTATTCATACCGTCCACCATCGGGGGGGGATTCATGACAAACCCAAATCATAC 120
QY 121 GAATGCAATTCATACCACTGCTTGAGTAACCCAGAAAGTTGAAGTACTTGTGAGAAAGC 180
DB 121 GAATGCAATTCATACCACTGCTTGAGTAACCCAGAAAGTTGAAGTACTTGTGAGAAAGC 180
QY 181 ATTGAACCCGGTTACATCTCCATGACATCTCTCTTCTTGACACAGTTTCTGCTAGC 240
DB 181 ATTGAACCCGGTTACATCTCCATGACATCTCTCTTCTTGACACAGTTTCTGCTAGC 240
QY 241 GAGTTGCGCAGAGGCTGGGTGGTCTCGGACAGTGAATCATCATCTGGGGTATCTT 300
DB 241 GAGTTGCGCAGAGGCTGGGTGGTCTCGGACAGTGAATCATCATCTGGGGTATCTT 300
QY 301 GGTCCATCTCAATGGAGATGATTCCTGCTGCAAAATTGACAGTTGATCAACAGAGATC 360
DB 301 GGTCCATCTCAATGGAGATGATTCCTGCTGCAAAATTGACAGTTGATCAACAGAGATC 360
QY 361 GAAAGATTCCGCAAGAACAGGCCATCTCTAGTTGGAAGATTGAGCAATCTCTACCA 420
DB 361 GAAAGATTCCGCAAGAACAGGCCATCTCTAGTTGGAAGATTGAGCAATCTCTACCA 420
QY 421 ATCTATGAGAGAGGTTGAGAGAGTGGGAGGCCATCTACTAACCCAGCTCTCGGAG 480
DB 421 ATCTATGAGAGAGGTTGAGAGAGTGGGAGGCCATCTACTAACCCAGCTCTCGGAG 480
QY 481 GAAATGCGTATTTCAATTCAACGACATGAAACAGCGCTTGACACAGCTATCCATTTTC 540
DB 481 GAAATGCGTATTTCAATTCAACGACATGAAACAGCGCTTGACACAGCTATCCATTTTC 540
QY 541 GCAGTCCAGAACTACCAAGTCTCTCTTCTCGGTACAGTTCAAGCAAGCTATCTTAC 600
DB 541 GCAGTCCAGAACTACCAAGTCTCTCTTCTCGGTACAGTTCAAGCAAGCTATCTTAC 600
QY 601 CTCAGCGGCTTCGAGAGCTTACGCTGTTTGGGCAAAAGTGGGGATTGATGCTGCAAC 660
DB 601 CTCAGCGGCTTCGAGAGCTTACGCTGTTTGGGCAAAAGTGGGGATTGATGCTGCAAC 660
QY 661 ATCAATAGCCGTTACCAACGACCTTACTAGGCTGATTGGAACCTACACGCAACGCTGT 720
DB 661 ATCAATAGCCGTTACCAACGACCTTACTAGGCTGATTGGAACCTACACGCAACGCTGT 720
QY 721 CGTTGGTACAACTGCGCTTGGAGGCTGTCTGGGGTCTGTGATTCTAGAGATTGGA 780
DB 721 CGTTGGTACAACTGCGCTTGGAGGCTGTCTGGGGTCTGTGATTCTAGAGATTGGA 780
QY 781 TACAACAGTTCAGAGAGAAATTGACCTTACAGATTTTGACATTTGTCTCTTCCG 840
DB 781 TACAACAGTTCAGAGAGAAATTGACCTTACAGATTTTGACATTTGTCTCTTCCG 840
QY 841 AACTATGACTCCAGAACTTACCTTATCCGTACAGTGTCCCACTTACAGAGAAATCTAT 900
DB 841 AACTATGACTCCAGAACTTACCTTATCCGTATCCGTACAGTGTCCCACTTACAGAGAAATCTAT 900
QY 901 ACTAACCCAGTCTTGAGAACTTGAACGCTTCCGTGTTCTGCCCAAGTATCGAA 960
DB 901 ACTAACCCAGTCTTGAGAACTTGAACGCTTCCGTGTTCTGCCCAAGTATCGAA 960
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DB 901 ACTAACCCAGTCTTGAGAACTTGAACGCTTCCGTGTTCTGCCCAAGTATCGAA 960
QY 961 GGTCCATTCAGAGAGCCACACTTGATGATCATCTTGAAACAGATTAATATATACCCGAT 1020
DB 961 GGTCCATTCAGAGAGCCACACTTGATGATCATCTTGAAACAGATTAATATATACCCGAT 1020
QY 1021 GCTCAGAGAGAGATTAATCTGCTGTAACACCAATGATCATGCTCTCCAGTTGGATTTC 1080
DB 1021 GCTCAGAGAGAGATTAATCTGCTGTAACACCAATGATCATGCTCTCCAGTTGGATTTC 1080
QY 1081 AGCGGGCCGAGTTTACTTCTCTTCTATGAACTATGGAAGAGCGCGCTCCACAA 1140
DB 1081 AGCGGGCCGAGTTTACTTCTCTTCTATGAACTATGGAAGAGCGCGCTCCACAA 1140
QY 1141 CGTATCGTTCTCAATAGGTGCAAGGCTGTCTACAGAACTTGTCTTCCACTTGTACGA 1200
DB 1141 CGTATCGTTCTCAATAGGTGCAAGGCTGTCTACAGAACTTGTCTTCCACTTGTACGA 1200
QY 1201 AGACCTTCAATATCGGTATCAACACAGCACTTCCGTTCTTGACGGAACAGATTTC 1260
DB 1201 AGACCTTCAATATCGGTATCAACACAGCACTTCCGTTCTTGACGGAACAGATTTC 1260
QY 1261 GCTTATGGAACCTTCTTAACCTTGCAATCCGCTGTGTTACAGAAAGAGCGGAT 1320
DB 1261 GCTTATGGAACCTTCTTAACTTGCAATCCGCTGTGTTACAGAAAGAGCGGAT 1320
QY 1321 TCTTGGACGAAATCCACACAGAACAAATATGACACCCAGCAAGATTTCTCCAC 1380
DB 1321 TCTTGGACGAAATCCACACAGAACAAATATGACACCCAGCAAGATTTCTCCAC 1380
QY 1381 AGTTGAGCAAGTGTCCATGTTCCGTTCCGATTCAGCAACAGTTCCGTGATCATC 1440
DB 1381 AGTTGAGCAAGTGTCCATGTTCCGTTCCGATTCAGCAACAGTTCCGTGATCATC 1440
QY 1441 AGAGCTCTTATGTTCTATGATGATTCATGATGCTAGTCAATATGATCTCTCC 1500
DB 1441 AGAGCTCTTATGTTCTATGATGATTCATGATGCTAGTCAATATGATCTCTCC 1500
QY 1501 TCTCAAAATCAACCAATTCCTCAATGACCAAGCTTCTAACTTGGATCTGAACTTCTGTC 1560
DB 1501 TCTCAAAATCAACCAATTCCTCAATGACCAAGCTTCTAACTTGGATCTGAACTTCTGTC 1560
QY 1561 GTGAAGGACAGGCTTCAAGAGGATGATTTCTTGAGAACTTCTCTGCGCAGATT 1620
DB 1561 GTGAAGGACAGGCTTCAAGAGGATGATTTCTTGAGAACTTCTCTGCGCAGATT 1620
QY 1621 AGCACCCTCAGAGTTACATCAGCAACCTTCTCAAGATATCGTGAGGATTCTGT 1680
DB 1621 AGCACCCTCAGAGTTACATCAGCAACCTTCTCAAGATATCGTGAGGATTCTGT 1680
QY 1681 TACGATCTACCACTTACCTTGCAATTCACACCTTCAATCGACGGAAGCTTATCATAG 1740
DB 1681 TACGATCTACCACTTACCTTGCAATTCACACCTTCAATCGACGGAAGCTTATCATAG 1740
QY 1741 GGTAACTTCTCCGCAACATGTCAGAGGCACTTCAATCCGAGCTTGAGAAC 1800
DB 1741 GGTAACTTCTCCGCAACATGTCAGAGGCACTTCAATCCGAGCTTGAGAAC 1800
QY 1801 GTGCGTTTCACTACCTTCTTCAACTTCTTAAAGGATCAAGCTTTTACCTTAGCGCT 1860
DB 1801 GTGCGTTTCACTACCTTCTTCAACTTCTTAAAGGATCAAGCTTTTACCTTAGCGCT 1860
QY 1861 CATGTGTCAATTTCTGCAATGAAGTGAATTAACCGTATTTGAGTTTGTCTGCGGAA 1920
DB 1861 CATGTGTCAATTTCTGCAATGAAGTGAATTAACCGTATTTGAGTTTGTCTGCGGAA 1920
QY 1921 GTTACTTTCAGGCTGAGTACTGGAATTCA 1951
DB 1921 GTTACTTTCAGGCTGAGTACTGGAATTCA 1951
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RESULT 8
AAA75466

QY 1475 CTGAGTTCACAAATATCATCTCTCTCAATACCCAAATCCCATGACCAAGTCTA 1534
 DB 2400 CTGAGTTCACAAATATCATCTCTCTCAATACCCAAATCCCATGACCAAGTCTA 2459
 QY 1535 CTAACCTTGATCTGGAACTTCTGTCTGTAAGGACCGAGCTTCAACAGAGGTGATATTC 1594
 DB 2460 CTAACCTTGATCTGGAACTTCTGTCTGTAAGGACCGAGCTTCAACAGAGGTGATATTC 2519
 QY 1595 TTAGAAGAACTTCTCTGCGACGATATAGCACTCTAGAGTTATACATCATGACCACTT 1654
 DB 2520 TTAGAAGAACTTCTCTGCGACGATATAGCACTCTAGAGTTATACATCATGACCACTT 2579
 QY 1655 CTCAAGATATCTGTCTGAGATCTGTTACGATCTACCACTTACCTTACCTTCAACCT 1714
 DB 2580 CTCAAGATATCTGTCTGAGATCTGTTACGATCTACCACTTACCTTCAACCT 2639
 QY 1715 CCATCGACGGAAGGCTTATCATCATCGGTAATCTTCCGCAACCTGTCACAGCGGACGA 1774
 DB 2640 CCATCGACGGAAGGCTTATCATCATCGGTAATCTTCCGCAACCTGTCACAGCGGACGA 2699
 QY 1775 ACTTGCAATCCGCGAGCTTCAAGACCGTGGGTTTCACTACTCTTCAACTCTCTAAGC 1834
 DB 2700 ACTTGCAATCCGCGAGCTTCAAGACCGTGGGTTTCACTACTCTTCAACTCTCTAAGC 2759
 QY 1835 GATCAAGGCTTTCACCCCTTAGCGCTCATGTGTTCAATCTTGCAATGAGTATCATTTG 1894
 DB 2760 GATCAAGGCTTTCACCCCTTAGCGCTCATGTGTTCAATCTTGCAATGAGTATCATTTG 2819
 QY 1885 ACCGATATGAGTTTGTGCTTCCGCAAGTTACTTGGAGCTGAGTACTGAGATTCATGC 1954
 DB 2820 ACCGATATGAGTTTGTGCTTCCGCAAGTTACTTGGAGCTGAGTACTGAGATTCATGC 2879
 QY 1955 T 1955
 DB 2880 T 2880

RESULT 9
 AAD06314
 ID AAD06314 standard; DNA; 7378 BP.
 AC AAD06314;
 XX
 DT 10-AUG-2001 (first entry)
 XX
 DE Plasmid pZO1502 comprising Btk and Pat expression cassettes.
 XX
 KW Transgenic maize; expression cassette; 35S promoter; nopaline synthetase;
 KW NOS terminator; alcohol dehydrogenase intron; CryIab toxin;
 KW foodstuffs preparation; phosphinothricin acetyl transferase; PAT;
 KW Plasmid pZO1502; ds.
 XX
 OS Chimeric - Cauliflower mosaic virus.
 OS Chimeric - Zea mays.
 OS Chimeric - Streptomyces sp.
 OS Chimeric - Bacillus thuringiensis.
 XX
 PN US6222104-B1.
 XX
 PD 24-APR-2001.
 XX
 PF 13-APR-1999; 99US-0291238.
 XX
 PR 09-NOV-1994; 94US-0336627.
 PR 22-AUG-1996; 96US-0716836.
 PR 14-MAR-1997; 97US-0818573.
 PR 13-MAR-1998; 98US-0042426.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 PI Mettler IU, Krier M, Mies D;

DR. WPI: 2001-327266/34.
 XX
 PT Novel transgenic maize seed for hybrid maize plant production,
 PT comprising expression cassette linked operably with CAMV 35S promoter,
 PT alcohol dehydrogenase intron, insecticidal CryIab toxin gene or NOS
 PT terminator
 XX
 PS Example 1: Column 25-32; 24pp; English.
 XX
 CC The present invention relates to transgenic maize seed for hybrid maize
 CC plant production, comprising an expression cassette linked operably with
 CC constitutive Cauliflower mosaic virus (CaMV) 35S promoter, an alcohol
 CC dehydrogenase intron, a DNA encoding an insecticidal
 CC Bacillus thuringiensis (Bt) CryIab toxin and a nopaline synthetase (NOS)
 CC terminator. The transgenic maize seed is used in maize cultivation
 CC methods for propagating hybrid maize seeds and for growing hybrid maize
 CC plants. The maize is also used in foodstuffs preparation for animal or
 CC human consumption. The inbred maize line NP948 of the invention has
 CC reduced level of fungal toxins, hence suitable for foodstuffs
 CC preparation. Yield is high. Plant health is improved due to reduced
 CC stalk rot. Grain test weight is high and the rate of grain dry down is
 CC reduced. The present sequence is plasmid pZO1502. The plasmid
 CC comprises the base plasmid vector, an expression cassette for the Bt
 CC kunitzaki gene and an expression cassette for the Pat gene, which is
 CC related to the invention.
 XX
 SQ Sequence 7378 BP; 1917 A; 1803 C; 1719 G; 1939 T; 0 other;
 Query Match 66.3%; Score 1848.2; DB 22; Length 7378;
 Best local similarity 99.6%; Pred. No. 0;
 Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
 QY 95 CCATGACCAACCAACCAACATCAACGATGATTCATCACTGCTTGAATACCCAG 154
 DB 1020 CCATGACCAACCAACCAACATCAACGATGATTCATCACTGCTTGAATACCCAG 1079
 QY 155 AAGTTGAAGTACTTGTGTGAGAGACGATTGAAACCGGTTACCTCCATGACATCTCT 214
 DB 1080 AAGTTGAAGTACTTGTGTGAGAGACGATTGAAACCGGTTACCTCCATGACATCTCT 1139
 QY 215 TGTCTTGTGACACAGTTTCTGTCTGCGAGATTCGTCAGAGTCTGGGTTGTTCTGGAC 274
 DB 1140 TGTCTTGTGACACAGTTTCTGTCTGCGAGATTCGTCAGAGTCTGGGTTGTTCTGGAC 1199
 QY 275 TAGTTGACATCATCTGGGGTATCTTGTGTCATCTCAATGAGATGATTCCTGTGCAAA 334
 DB 1200 TAGTTGACATCATCTGGGGTATCTTGTGTCATCTCAATGAGATGATTCCTGTGCAAA 1259
 QY 335 TTGAGCAATTGATCAACCAAGATTCGAAGATTCCGACGACCAAGCCATCTCTAGGT 394
 DB 1260 TTGAGCAATTGATCAACCAAGATTCGAAGATTCCGACGACCAAGCCATCTCTAGGT 1319
 QY 395 TGGAAAGATTGAGCAATCTCTACCAATCTTATGAGAGAGCTTGAGAGAGGGGAAGCG 454
 DB 1320 TGGAAAGATTGAGCAATCTCTACCAATCTTATGAGAGAGCTTGAGAGAGGGGAAGCG 1379
 QY 455 ATCTTACTTAACCAAGCTCTCCGCGAGGAATGCGTATTCATTCGAACGATGAACAGCG 514
 DB 1380 ATCTTACTTAACCAAGCTCTCCGCGAGGAATGCGTATTCATTCGAACGATGAACAGCG 1439
 QY 515 CTTTGACCAAGCTATCCCATTTGTTGCGAGTCCGAAGTACCAAGTTCTCTTGTCCG 574
 DB 1440 CTTTGACCAAGCTATCCCATTTGTTGCGAGTCCGAAGTACCAAGTTCTCTTGTCCG 1499
 QY 575 TGTAGCTTCAAGCAAGCTATCTTCAAGCTCAGCGTCTTGAGAGTTAGCTGTTGGGC 634
 DB 1500 TGTAGCTTCAAGCAAGCTATCTTCAAGCTCAGCGTCTTGAGAGTTAGCTGTTGGGC 1559
 QY 635 AAAGTGGGATTCGATGCTGCAACCATCAATAGCCGTTTACACGACCTTACTAGCTGA 694
 DB 1560 AAAGTGGGATTCGATGCTGCAACCATCAATAGCCGTTTACACGACCTTACTAGCTGA 1619
 QY 695 TTGGAATAACACGACGACGCTGTGTTGTGTACAAACACTGCGCTTGGAGCGTGTCTGG 754

D	b	1620	TTGGAAACTACACCGACCAACCGCTTTCGTTGGTACAAACCTGCGTTGAGCGGTCTCGGG	1679
O	y	755	GTCTGATTTCTAGAGATTGGATTAGATACAAACAGTTCAAGAGAGAAATGACCTTCAACG	814
D	b	1680	GTCTGATTTCTAGAGATTGGATTAGATACAAACAGTTCAAGAGAGAAATGACCTTCAACG	1739
O	y	815	TTTTTGACAATTGATCTCTCTCTTCCCGAATATGACTCAGAAACCTACCTATCCGTACAG	874
D	b	1740	TTTTTGACATTGTGTCTCTCTTCCCGAATATGACTCAGAAACCTACCTATCCGTACAG	1799
O	y	875	TGTCCTCAACTTACAGAGAAATCTATATCTAACCCAGTTCCTTGAGAACTTCGACGGTAGCT	934
D	b	1800	TGTCCTCAACTTACAGAGAAATCTATATCTAACCCAGTTCCTTGAGAACTTCGACGGTAGCT	1859
O	y	935	TCGCTGCTTCTGCCAAGTATGCAAGGCTTCATCAGAGGCCCAACCTGATGACATCT	994
D	b	1860	TCGCTGCTTCTGCCAAGTATGCAAGGCTTCATCAGAGGCCCAACCTGATGACATCT	1919
O	y	995	TGAAACAGCTATACCTATCTACACCCGATGCTCACAGAGAGATATTACTGGTCTGACACCC	1054
D	b	1920	TGAAACAGCTATACCTATCTACACCCGATGCTCACAGAGAGATATTACTGGTCTGACACCC	1979
O	y	1055	AGATCAGAGGCTCTCCAGTTGGATTTCAGCGGGCCCGAGTTAACCTTTCCTCATAGGAA	1114
D	b	1980	AGATCAGAGGCTCTCTCAGTTGGATTTCAGCGGGCCCGAGTTAACCTTTCCTCATAGGAA	2039
O	y	1115	CTATGAGAAACGCGCGCTCACACAAACGATATGTTGCTCAACTAGTCAGGGTCTTACA	1174
D	b	2040	CTATGAGAAACGCGCGCTCACACAAACGATATGTTGCTCAACTAGTCAGGGTCTTACA	2099
O	y	1175	GAACCTGTCTTCCACCTTGTACAGAAAGCCCTTCAATATCGGTATCAACCAACGACAC	1234
D	b	2100	GAACCTGTCTTCCACCTTGTACAGAAAGCCCTTCAATATCGGTATCAACCAACGACAC	2159
O	y	1235	TTTCCGTTCTTGAAGGAACAGAGTTCCGCTATGGAACCTCTTCTATCTTGCACTCCGCTG	1294
D	b	2160	TTTCCGTTCTTGAAGGAACAGAGTTCCGCTATGGAACCTCTTCTATCTTGCACTCCGCTG	2219
O	y	1295	TTTACAGAAAGCGGAACCGTTGATTCCTTGACGAATATCCACACAGAAACAACATG	1354
D	b	2220	TTTACAGAAAGCGGAACCGTTGATTCCTTGACGAATATCCACACAGAAACAACATG	2279
O	y	1355	TGCCACCCAGGCAAGAGATTCTCCACAGGTTGAGCAGCTGTCCATGTTCCGTTCCGAT	1414
D	b	2280	TGCCACCCAGGCAAGAGATTCTCCACAGGTTGAGCAGCTGTCCATGTTCCGTTCCGAT	2339
O	y	1415	TCACCAACAGTTCCGTGACATCATCAGAGCTCCATATGTTCTCATTGCATTCATCGTAGT	1474
D	b	2340	TCACCAACAGTTCCGTGACATCATCAGAGCTCCATATGTTCTCATTGCATTCATCGTAGT	2399
O	y	1475	CTGAGTTCAACATATCATTCCTTCCTCTCAAAATCACCAATATCCATTTGACCAAGTCTA	1534
D	b	2400	CTGAGTTCAACATATCATTCCTTCCTCTCAAAATCACCAATATCCATTTGACCAAGTCTA	2459
O	y	1535	CTAAACCTTGGATCTGGAACCTTCTGTCTGTGAAGAACAAGGCTTCAACAGAGGTGATATTC	1594
D	b	2460	CTAAACCTTGGATCTGGAACCTTCTGTCTGTGAAGAACAAGGCTTCAACAGAGGTGATATTC	2519
O	y	1595	TTAGAGAACTTCTCTGCGCAGATTTAGAACCTTCAGAGTTAACATCACTGACACACTTT	1654
D	b	2520	TTAGAGAACTTCTCTGCGCAGATTTAGAACCTTCAGAGTTAACATCACTGACACACTTT	2579
O	y	1655	CTCAAGATATCGGTGACAGATTGGTTACGATCTACACATTAATCTGGAATTCACACCT	1714
D	b	2580	CTCAAGATATCGGTGACAGATTGGTTACGATCTACACATTAATCTGGAATTCACACCT	2639
O	y	1715	CCATGACGGAAGGCTTATCATCATCAGGGTAACTTCTCCGCAACCATGTCAAGCGGACCA	1774
D	b	2640	CCATGACGGAAGGCTTATCATCATCAGGGTAACTTCTCCGCAACCATGTCAAGCGGACCA	2699
O	y	1775	ACTTGCAATCCGGACGCTTACGAACCGTCCGTTTCACTACTCTTCAACTTCTTAACG	1834

Db	2700	ACTTGCAATCCGGAGCTTCAGAAACCGTCGGTTTCACCTACCTCCCTTCAACTTCTCTAACG	2754
Qy	1835	GATTAACCGTTTTCACCTTACCGCTCATGTGTTCAAATTCTCGCAATGAACTGTACATTG	1894
Db	2760	GATTCACACGGTTTTCACCTTACCGCTCATGTGTTCAAATTCTCGCAATGAACTGTACATTG	2819
Qy	1895	ACCGTATTGAGTTTGTCTGCTGCGCAAGTTACCTTCGAGCGTGAATCTGAAATTCATGC	1954
Db	2820	ACCGTATTGAGTTTGTCTGCTGCGCAAGTTACCTTCGAGCGTGAATCTGAAATTCATGCA	2879
Qy	1955	T	1955
Db	2880	T	2880
RESULT 10			
AAD06368			
ID	AAD06368	standard; DNA; 7378 BP.	
XX	AAD06368;		
AC			
XX	10-AUG-2001	(first entry)	
DT			
XX			
DE	Plasmid pZO1502 comprising Bck and Pat gene expression cassettes.		
XX			
KW	Maize; expression cassette; 35S promoter; alcohol dehydrogenase intron;		
KW	crystal 1ab; CryIab toxin; phosphinothricin acetyl transferase; PAT;		
KW	nopaline synthase; NOS terminator; aflatoxin; food material;		
XX	sweet corn; human food; plasmid pZO1502; ds.		
OS	Chimeric - Zea mays.		
OS	Chimeric - Cauliflower mosaic virus.		
OS	Chimeric - Bacillus thuringiensis.		
OS	Chimeric - Streptomyces sp.		
XX			
FH	Key	location/Qualifiers	
FT	misc_feature	1022..2869	
FT	/tag= a		
FT	/note= "Corresponds to Bt CryIab toxin DNA"		
FT	misc_feature	4294..4845	
FT	/tag= b		
FT	/note= "Corresponds to Pat gene"		
FT	misc_feature	5269..6290	
FT	/tag= b		
FT	/note= "Corresponds to beta-lactamase gene"		
PN	US6229075-B1.		
XX			
PD	08-MAY-2001.		
XX			
PF	11-JUN-1999;	99US-0330760.	
XX			
PR	14-MAR-1997;	97US-0109808.	
PR	13-MAR-1998;	98US-0042426.	
XX			
PA	(NOVS) NOVARTIS AG.		
XX			
PI	Mettler ID, Plaisted DC, Grier SL, Houghton W, Gardiner M;		
DR	WPI; 2001-342708/36.		
XX			
PT	New maize (Zea mays) inbred line R412H (ATCC 209675), useful for		
PT	producing corn with reduced levels of toxins (e.g. the fungal		
PT	aflatoxin) and for preparing food materials for human or animal		
PT	consumption -		
XX			
PS	Example 1; Column 21-28; 30pp; English.		
XX			
CC	The present invention relates to maize inbred line R412H which comprises		
CC	a nucleic acid construct with two cassettes, which are transcribed in the		
CC	same direction. The expression cassette comprises a Cauliflower mosaic		
CC	virus (CAMV) 35S constitutive promoter operably linked to a maize alcohol		
CC	dehydrogenase intron, a DNA sequence of a gene encoding a		

CC Bacillus thuringiensis (Bt) crystal 1Ab (CryIAb) toxin or
 CC phosphinothricin acetyl transferase (PAT) and a nopaline synthase (NOS)
 CC terminator functional in plants. The maize indured line R412H is useful
 CC for producing corn with reduced levels of toxins (e.g. the fungal
 CC aflatoxin). This maize line is particularly useful for preparing food
 CC materials for human or animal consumption, e.g. sweet corn for
 CC packaging or fresh use as human food, or grain or silage made from field
 CC corn. The present sequence is plasmid p201502. The plasmid
 CC comprises the base plasmid vector and an expression cassette for the Btk
 CC gene and pat gene, which is related to the invention.

SO Sequence 7378 BP; 1917 A; 1803 C; 1719 G; 1939 T; 0 other:

Query Match 66.3%; Score 1848.2; DB 22; Length 7378;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 95 CCATGACACACACCCAAACATCAACGATTCCTTACACTGCTTGAGTAACCG 154
 DB 1020 CCATGACACACACCCAAACATCAACGATTCCTTACACTGCTTGAGTAACCG 1079
 QY 155 AAGTTGAAGTACTGGTGGAGACGATGAAACGGGTACACTCCATCGACATCTCT 214
 DB 1080 AAGTTGAAGTACTGGTGGAGACGATGAAACGGGTACACTCCATCGACATCTCT 1139
 QY 215 TGTCTTGACACAGTTTCTGCTCAGCGAGTTGCTGCGAGTGTGGATTCTCTCG 274
 DB 1140 TGTCTTGACACAGTTTCTGCTCAGCGAGTTGCTGCGAGTGTGGATTCTCTCG 1139
 QY 275 TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGGATGCAATTCCTG 334
 DB 1200 TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGGATGCAATTCCTG 1259
 QY 335 TTGACAGATTGATCAACAGAGATCGAAGAGTTGCGCAGGAACCGAGCCATCTAG 394
 DB 1260 TTGACAGATTGATCAACAGAGATCGAAGAGTTGCGCAGGAACCGAGCCATCTAG 1319
 QY 395 TGAAGATTGAGCAATCTCTCAAAATCTATGACAGAGCTTCAGAGTGGAGCG 454
 DB 1320 TGAAGATTGAGCAATCTCTCAAAATCTATGACAGAGCTTCAGAGTGGAGCG 1379
 QY 455 ATCTACTAACCCAGCTCTCCGCGAGAAATCCGATTCATTCAGACATGAACAG 514
 DB 1380 ATCTACTAACCCAGCTCTCCGCGAGAAATCCGATTCATTCAGACATGAACAG 1439
 QY 515 CTTGACACAGCTATCCCATTTGTCGAGTCCAGAACTACCAAGTTCTCTTGTGCG 574
 DB 1440 CTTGACACAGCTATCCCATTTGTCGAGTCCAGAACTACCAAGTTCTCTTGTGCG 1499
 QY 575 TGTAGCTTCAAGCAGCTAATCTTCACTCAGCGTCTTCGAGACGTTAGCGT 634
 DB 1500 TGTAGCTTCAAGCAGCTAATCTTCACTCAGCGTCTTCGAGACGTTAGCGT 1559
 QY 635 AAAGGTGGGATTCGATGCTGCAACATCAATAGCCGTTACAGCACTTACTAGGCT 694
 DB 1560 AAAGGTGGGATTCGATGCTGCAACATCAATAGCCGTTACAGCACTTACTAGGCT 1619
 QY 695 TTGGAATACACACGACGCTGTTGCTGTTCAACAACACTGCTGGAGCGTGTGCG 754
 DB 1620 TTGGAATACACACGACGCTGTTGCTGTTCAACAACACTGCTGGAGCGTGTGCG 1679
 QY 755 GTCTGATTTAGAGATTGATTAGATCAACCACTTCAGAGAGAAATTGACCTCAG 814
 DB 1680 GTCTGATTTAGAGATTGATTAGATCAACCACTTCAGAGAGAAATTGACCTCAG 1739
 QY 815 TTTTGAATGTTGCTCTCTTCCGGAAGTATGACTCCAGAACCTTACCTTACG 874
 DB 1740 TTTTGAATGTTGCTCTCTTCCGGAAGTATGACTCCAGAACCTTACCTTACG 1799
 QY 875 TGTCCCACTTACAGAGAAATCTATCTAATCCAGATTCTTGAGAACTTCAAGT 934
 DB 1800 TGTCCCACTTACAGAGAAATCTATCTAATCCAGATTCTTGAGAACTTCAAGT 1859

QY 935 TCCGTGTTCTGCCCAAGGATATCGAAGGCTTCATCAGAGACCCCACTTATGACATCT 994
 DB 1860 TCCGTGTTCTGCCCAAGGATATCGAAGGCTTCATCAGAGACCCCACTTATGACATCT 1919
 QY 995 TGAACACATATATCTATACACGATGCTCAGACAGAGAGATTTACTGCTGACACC 1054
 DB 1920 TGAACACATATATCTATACACGATGCTCAGACAGAGAGATTTACTGCTGACACC 1979
 QY 1055 AGATCATGAGCTCTCCAGTTGATTCAGCGGGCCGAGTTTACTCTTCTATAGAA 1114
 DB 1980 AGATCATGAGCTCTCCAGTTGATTCAGCGGGCCGAGTTTACTCTTCTATAGAA 2039
 QY 1115 CTATGGAAACCGCGCTCCACACAGATATCTGTTCTCACTATGCTCAGGCTCTACA 1174
 DB 2040 CTATGGAAACCGCGCTCCACACAGATATCTGTTCTCACTATGCTCAGGCTCTACA 2099
 QY 1175 GAACCTTGCTCCACCTGTACAGAGACCCCTCAATATCCGATCAACACAGCAAC 1234
 DB 2100 GAACCTTGCTCCACCTGTACAGAGACCCCTCAATATCCGATCAACACAGCAAC 2159
 QY 1235 TTTCCGTTCTTGACGGAACAGAGTTCCGCTATAGAACCTCTTCTTACTTGGCATCC 1294
 DB 2160 TTTCCGTTCTTGACGGAACAGAGTTCCGCTATAGAACCTCTTCTTACTTGGCATCC 2219
 QY 1295 TTTACAGAAAGCGGAAACGTTGATTTCTTGACGAAATCCACACAGAACCAATG 1354
 DB 2220 TTTACAGAAAGCGGAAACGTTGATTTCTTGACGAAATCCACACAGAACCAATG 2279
 QY 1355 TGCCACCGAGCAAGATTTCCCAAGGTTGACCGAGTTCATGCTCCGCTCCGAT 1414
 DB 2280 TGCCACCGAGCAAGATTTCCCAAGGTTGACCGAGTTCATGCTCCGCTCCGAT 2339
 QY 1415 TCAGCAACAGTTCGATGAGATCATCAGAGCTCTATGTTCTCATGATTCATGATG 1474
 DB 2340 TCAGCAACAGTTCGATGAGATCATCAGAGCTCTATGTTCTCATGATTCATGATG 2399
 QY 1475 CTGAGTTCAACAAATATCTTCTCTCTCAAAATCCCAATTCCTTACCAAGCTA 1534
 DB 2400 CTGAGTTCAACAAATATCTTCTCTCTCAAAATCCCAATTCCTTACCAAGCTA 2459
 QY 1535 CTAACCTTGAATCTGGAACCTTCTGCTGAAAGACAGAGCTTCACAGAGATATATC 1594
 DB 2460 CTAACCTTGAATCTGGAACCTTCTGCTGAAAGACAGAGCTTCACAGAGATATATC 2519
 QY 1595 TTAGAAGAACTTCTCTGCGCAGATTAGACACCTCAGAGTTAATCATCATGACCAT 1654
 DB 2520 TTAGAAGAACTTCTCTGCGCAGATTAGACACCTCAGAGTTAATCATCATGACCAT 2579
 QY 1655 CTCAAAGATATCTGTCAGGATTTGTTACGATCTACATTAATTTGCAATTCACACCT 1714
 DB 2580 CTCAAAGATATCTGTCAGGATTTGTTACGATCTACATTAATTTGCAATTCACACCT 2639
 QY 1715 CCATCGACGGAAGGCTATCAATCAGGTTAATCTCTCGCAACCATGCAAGCGGACAGA 1774
 DB 2640 CCATCGACGGAAGGCTATCAATCAGGTTAATCTCTCGCAACCATGCAAGCGGACAGA 2699
 QY 1775 ACTTGCAATCCGGAGCTTCAGAACCGTGGTTTCACTACTCTTCAACTTCTTAAG 1834
 DB 2700 ACTTGCAATCCGGAGCTTCAGAACCGTGGTTTCACTACTCTTCAACTTCTTAAG 2759
 QY 1835 GATCAAGGTTTTCACCTTACCGCTCATATGTTCAATTTGCGGAATCAAGTATCATG 1894
 DB 2760 GATCAAGGTTTTCACCTTACCGCTCATATGTTCAATTTGCGGAATCAAGTATCATG 2819
 QY 1895 ACCGATATGATTTGCTGCTCCGAAAGTAACTTCAAGGCTGAGTATGAAATTCATGC 1954
 DB 2820 ACCGATATGATTTGCTGCTCCGAAAGTAACTTCAAGGCTGAGTATGAAATTCATGC 2879
 QY 1955 T 1955
 DB 2880 T 2880

RESULT 11
AAF89825
ID AAF89825 standard; DNA; 7378 BP.
XX
AC AAF89825;
XX
DT 23-JUL-2001 (first entry)
XX
DE Nucleotide sequence of plasmid pZ01502.
XX
KW Maize; inbred line R660H; 35S constitutive promoter; Cry1Ab protein;
KW alcohol dehydrogenase; phosphinothricin acetyl transferase; chromosome 8;
KW Z1B3; UMC150a; Lepidoptera; Glutiosinate; sweet corn; fungal toxin; ds.
XX
OS Synthetic.
OS Bacillus thuringiensis.
XX
FH Key Location/Qualifiers
FT 1022..2869
FT /*tag= a
FT /product= "Cry1Ab; encodes AAB83922"
FT CDS 4294..4845
FT /*tag= b
FT /product= "Pat gene; encodes AAB83923"
XX
PN US6232533-B1.
XX
PD 15-MAY-2001.
XX
PF 09-JUN-1999; 99US-0328473.
XX
PR 14-MAR-1997; 97US-0109808.
PR 13-MAR-1998; 98US-0042426.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Mettler IJ, Plaisted DC, Griener SL, Houghton W, Gardiner M;
XX
DR WPI: 2001-335091/35.
DR P-PSDB; AAB83922, AAB83923.
XX
PT Novel seed of maize inbred line R372H, useful for producing inbred
PT maize plants which on crossing with other different maize plants
PT produce hybrid maize seeds and plants having resistance to insects and
PT herbicide
XX
PS Example 1; Column 21-28; 29pp; English.
XX
CC The specification describes seed and plants of maize inbred line R660H.
CC
CC The seed comprises two cassettes. The first cassette comprises a
CC cauliflower mosaic virus (CaMV) 35S constitutive promoter operably linked
CC to a maize alcohol dehydrogenase intron, a DNA sequence of a gene
CC encoding a Cry1Ab protein, and a terminator functional in plants. The
CC second cassette comprises a CaMV 35S promoter which functions in plant
CC cells operably linked to a maize alcohol dehydrogenase intron, a DNA
CC sequence of a gene encoding for phosphinothricin acetyl transferase, and
CC a terminator functional in plant. The two cassettes are transcribed in
CC the same direction and the nucleic acid construct is incorporated into
CC the seed's genome on chromosome 8 and near position 117, between markers
CC Z1B3 and UMC150a. The maize plants and seeds exhibit resistance to
CC Lepidopteran insects since they express the protein Cry1Ab in high
CC levels, and also exhibit resistance to non-selective herbicide
CC glufosinate. The transgenic maize is suited for preparation of food
CC materials for human or animal consumption e.g. sweet corn for packaging
CC or fresh use as a human food, or grain or silage made from field corn,
CC containing reduced levels of fungal toxins. The present sequence
CC represents plasmid pZ01502, which is used to produce transgenic maize
CC of the invention.
XX
SQ Sequence 7378 BP; 1917 A; 1803 C; 1719 G; 1939 T; 0 other;

Query Match 66.3%; Score 1848.2; DB 22; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;

Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;									
QY	95	CCATGACAAACAAACCAACATCAACGAATGCAATTCATACACTGCTTGAATACCCAG	154						
DB	1020	CCATGACAAACAAACCAACATCAACGAATGCAATTCATACACTGCTTGAATACCCAG	1079						
QY	155	AAGTTGAAGTACTTGGTGAAGAACGATCGAATCCGCTTACCTCCATGACATCTCT	214						
DB	1080	AAGTTGAAGTACTTGGTGAAGAACGATCGAATCCGCTTACCTCCATGACATCTCT	1139						
QY	215	TGCTCTTGAACAGCTTCTCTGCTCAAGAGTTCGGCAGGTCGGGTGGTCTCGGAC	274						
DB	1140	TGCTCTTGAACAGCTTCTCTGCTCAAGAGTTCGGCAGGTCGGGTGGTCTCGGAC	1139						
QY	275	TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGAGATCAATTCCTGGTGC	334						
DB	1200	TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGAGATCAATTCCTGGTGC	1259						
QY	335	TTGAGCAGTTGATTAACCAAGAGATCGAAGAGTTCCGACAGAACCCAGCCATCTTAG	394						
DB	1260	TTGAGCAGTTGATTAACCAAGAGATCGAAGAGTTCCGACAGAACCCAGCCATCTTAG	1319						
QY	395	TGGAAGATTGAGCAATCTCTACCAATCTATGACAGAGAGCTGACAGAGTGGAGCCG	454						
DB	1320	TGGAAGATTGAGCAATCTCTACCAATCTATGACAGAGAGCTGACAGAGTGGAGCCG	1379						
QY	455	ATCCTTAACCCAGCTCTCCGCGAGGAAATGCGTATTCATTCAGACGACATGAACAG	514						
DB	1380	ATCCTTAACCCAGCTCTCCGCGAGGAAATGCGTATTCATTCAGACGACATGAACAG	1439						
QY	515	CCTTGACCAAGCTATCCCATTTGTCGAGTCCGAACTACCAAGTCTCTCTTGTCCG	574						
DB	1440	CCTTGACCAAGCTATCCCATTTGTCGAGTCCGAACTACCAAGTCTCTCTTGTCCG	1499						
QY	575	TGTAGCTTCAAGCAGCTAATCTTCACTCAGCGGCTTCGAGAGTTAGAGCTTTGGGC	634						
DB	1500	TGTAGCTTCAAGCAGCTAATCTTCACTCAGCGGCTTCGAGAGTTAGAGCTTTGGGC	1559						
QY	635	AAAGTGGGGATTGATGCTGCAACCAATCAATAGCCGTTACACGACCTTACTAGCTGA	694						
DB	1560	AAAGTGGGGATTGATGCTGCAACCAATCAATAGCCGTTACACGACCTTACTAGCTGA	1619						
QY	695	TTGAAATACACCGACCAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	754						
DB	1620	TTGAAATACACCGACCAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1679						
QY	755	GTCCTGATTTAGAGATTGGATTGATTAACACCGAGTTGAGAGATTTGACCCCTCAG	814						
DB	1680	GTCCTGATTTAGAGATTGGATTGATTAACACCGAGTTGAGAGATTTGACCCCTCAG	1739						
QY	815	TTTTGACATTTGTTCTCTTCCGAACTATGACTCCGAACTTACCTTCCGTACAG	874						
DB	1740	TTTTGACATTTGTTCTCTTCCGAACTATGACTCCGAACTTACCTTCCGTACAG	1799						
QY	875	TGTCCCACTTACAGAGAAATCTATTAACCAAGCTTGAAGAACTTGAAGCTTACT	934						
DB	1800	TGTCCCACTTACAGAGAAATCTATTAACCAAGCTTGAAGAACTTGAAGCTTACT	1859						
QY	935	TCCGTGTTTGCACCAAGTATCGAAGGCTCCATCAGGAGCCCACTTGTGAGCATCT	994						
DB	1860	TCCGTGTTTGCACCAAGTATCGAAGGCTCCATCAGGAGCCCACTTGTGAGCATCT	1919						
QY	995	TGAACAGCATTAATTAACCAAGAGTCTCAAGAGAGAGATTAATCTGTTGTGACACC	1054						
DB	1920	TGAACAGCATTAATTAACCAAGAGTCTCAAGAGAGAGATTAATCTGTTGTGACACC	1979						
QY	1055	AGATCATGCTCTTCCAGTTGATTAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGG	1114						
DB	1980	AGATCATGCTCTTCCAGTTGATTAACCAAGGAGGAGGAGGAGGAGGAGGAGGAGG	2039						
QY	1115	CTATGGAGAAAGCGAGCTCACAACAGATATGTTGCTCACTAGAGTGTGCTAC	1174						
DB	2040	CTATGGAGAAAGCGAGCTCACAACAGATATGTTGCTCACTAGAGTGTGCTAC	2099						

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OY 1175 GAACCTGTCCTCCACCTTGATGACAGAGACCCCTTCAATATGCGTATCAACACGAGAAC 1234
DB 2100 GAACTTGTCTTCCACCTTGATGACAGAGACCCCTTCAATATGCGTATCAACACGAGAAC 2159
OY 1335 TTTCCGCTTCTGACGGAACAGAGTTCCGCTTATGGAACCTCTTCACTTTCGCAATCCGCTG 1294
DB 2160 TTTCCGCTTCTGACGGAACAGAGTTCCGCTTATGGAACCTCTTCACTTTCGCAATCCGCTG 2219
OY 1295 TTTACAGAAAGAGCGGAACCGGTGATTCCTTGAAGAAATCCCAACAGAAACAATG 1354
DB 2220 TTTACAGAAAGAGCGGAACCGGTGATTCCTTGAAGAAATCCCAACAGAAACAATG 2279
OY 1355 TGCCACCCGAGCAAGATTTCTCCACAGGTGAGGCAAGTTCATGTTCCGTTCCGAT 1414
DB 2280 TGCCACCCGAGCAAGATTTCTCCACAGGTGAGGCAAGTTCATGTTCCGTTCCGAT 2339
OY 1415 TCAGCAACAGTTCCGTCAGCATCATCAGAGCTCCTATGTTTCTCATGATTCATGTAATG 1474
DB 2340 TCAGCAACAGTTCCGTCAGCATCATCAGAGCTCCTATGTTTCTCATGATTCATGTAATG 2399
OY 1475 CTGAGTTCAACATATCATCTCTCTCTCAATATCCCAATCCATTGACCAAGTCTA 1534
DB 2400 CTGAGTTCAACATATCATCTCTCTCTCAATATCCCAATCCATTGACCAAGTCTA 2459
OY 1535 CTAACCTTGATCTGGAACCTTCTGTCGTAAGAAAGACAGGCTTCACAGAGGTGATTTTC 1594
DB 2460 CTAACCTTGATCTGGAACCTTCTGTCGTAAGAAAGACAGGCTTCACAGAGGTGATTTTC 2519
OY 1595 TTAAGAAAGCTTCTCTGCGCAAGATTAGCAACCTTCAGAGTTTAACTCATCACTGCACCACTTT 1654
DB 2520 TTAAGAAAGCTTCTCTGCGCAAGATTAGCAACCTTCAGAGTTTAACTCATCACTGCACCACTTT 2579
OY 1655 CTCAAGATATCGTGTCAGAGTTGTTGTTAGCATCAACATCACTTGAATTTCCACACTT 1714
DB 2580 CTCAAGATATCGTGTCAGAGTTGTTGTTAGCATCAACATCACTTGAATTTCCACACTT 2639
OY 1715 CCATGACGGAAGGCTTATCATATCAGGTTAACTTCTCCGCAACCATGTCAGAGCGGACCA 1774
DB 2640 CCATGACGGAAGGCTTATCATATCAGGTTAACTTCTCCGCAACCATGTCAGAGCGGACCA 2699
OY 1775 ACTTGCAATCCGCGACGCTTCAGAACCGTTCGTTTCACTTCTTCACTTCTTAACG 1834
DB 2700 ACTTGCAATCCGCGACGCTTCAGAACCGTTCGTTTCACTTCTTCACTTCTTAACG 2759
OY 1835 GATCAAGGTTTTCACCCCTTAGCGCTCATGTTGTAATTCGGAATGAGTACATTG 1894
DB 2760 GATCAAGGTTTTCACCCCTTAGCGCTCATGTTGTAATTCGGAATGAGTACATTG 2819
OY 1895 ACCGTAATGAGTTTGTGCTGCGGAGTTTACCTTCGAGGCTGAGTACGAGATTCATGC 1954
DB 2820 ACCGTAATGAGTTTGTGCTGCGGAGTTTACCTTCGAGGCTGAGTACGAGATTCATGC 2879
OY 1955 T 1955
DB 2880 T 2880

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RESULT 12

AAf89834 ID AAF89834 standard; DNA; 7378 BP.

AAf89834;

23-JUN-2001 (first entry)

Nucleotide sequence of plasmid pZ01502.

Maize; Inbred line R660H; 35S constitutive promoter; CryIAb protein;
alcohol dehydrogenase; phosphinothricin acetyl transferase; chromosome 8;
Z1B3; UMC150a; Lepidoptera; glufosinate; sweet corn; fungal toxin; ds.
Synthetic.

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OS Bacillus thuringiensis.
XX Key Location/Qualifiers
FH CDS 1022..2869
FT CDS /*tag= a
FT CDS /product= "CryIAb; encodes AAB83924"
FT CDS 4294..4845
FT CDS /*tag= b
FT CDS /product= "Pat gene; encodes AAB83925"
XX US6232534-B1.
XX 15-MAY-2001.
XX 11-JUN-1999; 99US-0330737.
XX 14-MAR-1997; 97US-0818573.
XX 13-MAR-1998; 98US-0042426.
XX (NOVS ) NOVARTIS AG.
XX Mettler IU, Plaisted DC, Grier SL, Houghton W, Gardiner M;
XX WPI; 2001-335092/35.
XX P-PSDB; AAB83924, AAB83925.
XX Novel seed of maize inbred line R660H, useful for producing inbred
XX maize plants which on crossing with other different maize plants
XX produce hybrid maize seeds and plants having resistance to insects and
XX herbicide -
XX Example 1; Column 23-32; 24pp; English.
XX The specification describes seed and plants of maize inbred line R660H.
XX The seed comprises two cassettes. The first cassette comprises a
XX cauliflower mosaic virus (CaMV) 35S constitutive promoter operably linked
XX to a maize alcohol dehydrogenase intron, a DNA sequence of a gene
XX encoding a CryIAb protein, and a terminator functional in plants. The
XX second cassette comprises a CamV 35S promoter which functions in plant
XX cells operably linked to a maize alcohol dehydrogenase intron, a DNA
XX sequence of a gene encoding for phosphinothricin acetyl transferase, and
XX a terminator functional in plant. The two cassettes are transcribed in
XX the same direction and the nucleic acid construct is incorporated into
XX the seed's genome on chromosome 8 and near position 117, between markers
XX Z1B3 and UMC150a. The maize plants and seeds exhibit resistance to
XX lepidopteran insects since they express the protein CryIAb in high
XX levels, and also exhibit resistance to non-selective herbicide
XX glufosinate. The transgenic maize is suited for preparation of food
XX materials for human or animal consumption e.g. sweet corn for packaging
XX or fresh use as a human food, or grain or silage made from field corn,
XX containing reduced levels of fungal toxins. The present sequence
XX represents plasmid pZ01502, which is used to produce transgenic maize
XX of the invention.
XX Sequence 7378 BP; 1917 A; 1803 C; 1719 G; 1939 T; 0 other:
SQ
Query Match 66.3%; Score 1848.2; DB 22; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
OY 95 CCATGACACAAACCCCAACATCAACGAATGCTTCCATACACTGCTTGAATACCCAG 154
DB 1020 CCATGACACAAACCCCAACATCAACGAATGCTTCCATACACTGCTTGAATACCCAG 1079
OY 155 AAGTGAAGTCTTGCGGAGAGACGATTTGAAACCGGTTTACACTCCATCGACATCTCCT 214
DB 1080 AAGTGAAGTCTTGCGGAGAGACGATTTGAAACCGGTTTACACTCCATCGACATCTCCT 1139
OY 215 TGTCTTGACACAGTTTCTGCTCAGCGAGTTGTCGACGAGTCTGCTGCTTCTTGCGAG 274
DB 1140 TGTCTTGACACAGTTTCTGCTCAGCGAGTTGTCGACGAGTCTGCTGCTTCTTGCGAG 1199
OY 275 TAGTTGACATCATCTGGGCTATCTTGTGTCATCTCAATGGGATGCACTTCCGTGCGAA 334

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Db	1200	TAAGTTGACATCATCTGGGGATCTCTTGGTCCATCTCAATGGAGATGCAATTCCTGGTGCAAA	1259
Qy	335	TTGAGCAGCTTGATCAACACGAGGATTCGAAAGGTTCCGCACGAAACACGAGCCATCTTAGT	394
Db	1260	TTGAGCAGCTTGATCAACACGAGGATTCGAAAGGTTCCGCACGAAACACGAGCCATCTTAGT	1319
Qy	395	TGGAAGGATTGAGCAATCTCTTACCAAACTATATGAGAGAGCTTCAGAGTGGGAACCG	454
Db	1320	TGGAAGGATTGAGCAATCTCTTACCAAACTATATGAGAGAGCTTCAGAGTGGGAACCG	1379
Qy	455	ATCTTACTAACCCAGCTCTCCGCGAGGAAATGGCTATTCAATTGAACGATGAAACGCG	514
Db	1380	ATCTTACTAACCCAGCTCTCCGCGAGGAAATGGCTATTCAATTGAACGATGAAACGCG	1439
Qy	515	CCTTGACCAACAGCTATCCCATTTGTTGCGAGTCCAGAACTACCAAGTTCCTCTCTGACG	574
Db	1440	CCTTGACCAACAGCTATCCCATTTGTTGCGAGTCCAGAACTACCAAGTTCCTCTCTGACG	1499
Qy	575	TGTAAGTTCAAGCAGCTAATCTTCAACCTCAAGCGTGCTTCGAGAGTTAGCGTGTGGG	634
Db	1500	TGTAAGTTCAAGCAGCTAATCTTCAACCTCAAGCGTGCTTCGAGAGTTAGCGTGTGGG	1559
Qy	635	AAAGTGGGGATTGGATGCTGCAACCAATCAATACCCTGTACAAAGACCTTACTAGGCTGA	694
Db	1560	AAAGTGGGGATTGGATGCTGCAACCAATCAATACCCTGTACAAAGACCTTACTAGGCTGA	1619
Qy	695	TTGGAACCTACACGCAACGACGCTGTGCGTTGGTCAACACTGGCTGGAAGCTGTGCG	754
Db	1620	TTGGAACCTACACGCAACGACGCTGTGCGTTGGTCAACAACCTGGCTGGAAGCTGTGCG	1679
Qy	755	GTCTCTGATTCTAGAGATTGATTAATCAACAACGATTCAAGAGAAATTGACCCCTCAG	814
Db	1680	GTCTCTGATTCTAGAGATTGATTAATCAACAACGATTCAAGAGAAATTGACCCCTCAG	1739
Qy	815	TTTTTGACATTGTGTCTCTCTTCCCGAAGTATGACTCGAAGACCTTACCTTACCTGTACG	874
Db	1740	TTTTTGACATTGTGTCTCTCTTCCCGAAGTATGACTCGAAGACCTTACCTTACCTGTACG	1799
Qy	875	TGTCCCAACCTTACACGAGAAATCTATATACTAACCCAGTCTTGAGAACTTCGACGGTAGT	934
Db	1800	TGTCCCAACCTTACACGAGAAATCTATATACTAACCCAGTCTTGAGAACTTCGACGGTAGT	1859
Qy	935	TCCGTGGTTCGCCCAAGGTAATCGAAGGCTCCATCAGAGGCCACACCTTGATGACATCT	994
Db	1860	TCCGTGGTTCGCCCAAGGTAATCGAAGGCTCCATCAGAGGCCACACCTTGATGACATCT	1919
Qy	995	TGAAACAGATTAATACTTACAACCGATGCTCACAGAGGAGATTTACTGTCTGACAC	1054
Db	1920	TGAAACAGATTAATACTTACAACCGATGCTCACAGAGGAGATTTACTGTGTGACAC	1979
Qy	1055	AGATCATGCGCTCTCCAGTTGGATTCAAGCGGGCCGAAATTAACCTTCCTCTATGAAA	1114
Db	1980	AGATCATGCGCTCTCTCAATGAGATTCAAGCGGGCCGAAATTAACCTTCCTCTATGAAA	2039
Qy	1115	CTATGGAAGAACGCGCTCCACAACCAACTATGTTGCTCAACTAGAGTCAAGGATGTTACA	1174
Db	2040	CTATGGAAGAACGCGCTCCACAACCAAGTATGTTGCTCAACTAGAGTCAAGGATGTTACA	2099
Qy	1175	GAACTTGTCTTCCACTTGTATCAGAAAGCCCTTCAATATGGTATCAACAACGACAA	1234
Db	2100	GAACTTGTCTTCCACTTGTATCAGAAAGCCCTTCAATATGGTATCAACAACGACAA	2159
Qy	1235	TTTCCGTTCTTGAAGGAAACAGGTTGGCTATGGAACCTCTTCAACTTGGCATCCGCTG	1294
Db	2160	TTTCCGTTCTTGAAGGAAACAGGTTGGCTATGGAACCTCTTCAACTTGGCATCCGCTG	2219
Qy	1295	TTTACAGAAAGACGGAACCGTTGATCTCTTGGAGAAATCCACACAGAAACAACATG	1354
Db	2220	TTTACAGAAAGACGGAACCGTTGATCTCTTGGAGAAATCCACACAGAAACAACATG	2279
Qy	1355	TGCAACCAAGGCAAGATTCTTCCACAGTTGAGCCACGTCATCATGTTCCGTTCCGAT	1414

Db	2280	TGCCACCCAGGCAAGATTTCTCCACAGGTTAGACCAAGTGTGCATGTTCCGTTCCGGAT	2339
Oy	1415	TCAGCAACAGTTCCTCGTAGCATCATCAGAGCTCCTATGTTCTCATGGATTCACTGTAGTG	1474
Db	2340	TCAGCAACAGTTCCTCGTAGCATCATCAGAGCTCCTATGTTCTCATGGATTCACTGTAGTG	2399
Oy	1475	CTGAGTTCAACAAATATCATTCCTTCCCTCTCAAAATCAACCCAAATCCCATTTGACCAAGCTA	1534
Db	2400	CTGAGTTCAACAAATATCATTCCTTCCCTCTCAAAATCAACCCAAATCCCATTTGACCAAGCTA	2459
Oy	1535	CTAACCTTGGATCTGGAACCTTCTGTCCGTGAAGAAGACAGGCTTTCACAGAGAGTATATTC	1594
Db	2460	CTAACCTTGGATCTGGAACCTTCTGTCCGTGAAGAAGACAGGCTTTCACAGAGAGTATATTC	2519
Oy	1595	TTAGAGAAGTCTCTCTGGCCAGATTAGACACCTCTCAGAGTTAACAATCATGACCACTTT	1654
Db	2520	TTAGAGAAGTCTCTCTGGCCAGATTAGACACCTCTCAGAGTTAACAATCATGACCACTTT	2579
Oy	1655	CTCAAAGTATTCGTGTACAGATTGCTTAAGCATATACCAATTAATTGCAATTCACACCT	1714
Db	2580	CTCAAAGTATTCGTGTACAGATTGCTTAAGCATATACCAATTAATTGCAATTCACACCT	2639
Oy	1715	CCATCGACGGAAGGCTCATCAATCAGGGTAACTTCTCCGCACACATGTCAAAGCGGACGA	1774
Db	2640	CCATCGACGGAAGGCTCATCAATCAGGGTAACTTCTCCGCACACATGTCAAAGCGGACGA	2699
Oy	1775	ACTTGCAATCCGGAGCTTCAGAACGCGTGGTTTCACTACTCTCTTCAACTCTTCTAACG	1834
Db	2700	ACTTGCAATCCGGAGCTTCAGAACGCGTGGTTTCACTACTCTCTTCAACTCTTCTAACG	2759
Oy	1835	GATCAAGCGTTTTCACCTTAAGCGCTCATGTGTTCAATTCGCGCAATGAATGTACATTG	1894
Db	2760	GATCAAGCGTTTTCACCTTAAGCGCTCATGTGTTCAATTCGCGCAATGAATGTACATTG	2819
Oy	1895	ACCGTATGAGTTTGTGCTGCTCGCAAGTTACCTTCGAGGCTGAGTACTGAGAAATTCAATG	1954
Db	2820	ACCGTATGAGTTTGTGCTGCTCGCAAGTTACCTTCGAGGCTGAGTACTGAGAAATTCAATG	2879
Oy	1955	T 1955	
Db	2880	T 2880	
RESULT 13			
ABL57440			
ID	ABL57440	standard; DNA; 7378 BP.	
XX	ABL57440;		
XX	12-AUG-2002	(first entry)	
XX	Plasmid pZO1502 encoding insect and herbicide resistance in maize.		
XX	Maize; crop improvement; transgenic plant; disease resistance;		
KW	insect resistance; herbicide resistance; pZO1502; ds.		
OS	Chimeric - Zea mays.		
OS	Chimeric - Cauliflower mosaic virus.		
OS	Chimeric - Streptomyces sp.		
XX	Chimeric - Bacillus thuringiensis kurstaki.		
PN	US6329575-B1.		
XX	11-DEC-2001.		
XX	09-JUN-1999;	99US-0329169.	
XX	14-MAR-1997;	97US-109808P.	
XX	13-MAR-1998;	98US-0042426.	
PA	(SYGN) SYNGENTA PARTICIPATIONS AG.		
XX	Mettler IU, Mies D.		

XX WPI; 2002-121141/16.
DR New maize inbred line 2227BT, ATCC 203942, useful for animal and human
XX nutrition, contains genes for resistance to insects and herbicide
PT Example 1; Column 25-32; 24pp; English.
XX
PS The present sequence is the nucleotide sequence of plasmid pZ01502
XX (ATCC 209682). The plasmid includes an expression cassette for
CC Bacillus thuringiensis kurstaki CryIAb crystal protein and an
CC expression cassette for phosphinothricin acetyltransferase (see
CC also ABL5/432-39). Seed of maize inbred line 2227BT (ATCC 203942)
CC is claimed, which comprises a nucleic acid construct comprising
CC these 2 expression cassettes transcribed in the same direction and
CC incorporated into the seed's genome on chromosome 8, near position
CC 117, between markers Z1B3 and UMC150a. Also claimed are a maize
CC plant of inbred line 2227BT, its pollen, ovaries and other plant
CC parts, as well as hybrid seed produced by crossing the plant with
CC an inbred maize plant of different genotype. The nucleic acid
CC construct imparts resistance to phosphinothricin (glyphosate)
CC herbicide and to insects, particularly European corn borer
CC (*Ostrinia nubilalis*). Southwestern corn borer (*Diatraea grandiosella*)
CC and Fall armyworm (*Spodoptera frugiperda*). Grain and silage
CC produced from the new plants have reduced contents of aflatoxin,
CC possibly because the insect resistance provided by CryIAb reduces
CC opportunistic fungal infections.
XX
SQ Sequence 7378 BP; 1917 A; 1803 C; 1719 G; 1939 T; 0 other:
Query Match 66.3%; Score 1848.2; DB 24; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 95 CCATGGAAACAAACCCAAACATCAACGAATGATTCATCAACCTGTTAGTAAACCCAG 154
DB 1020 CCATGGAAACAAACCCAAACATCAACGAATGATTCATCAACCTGTTAGTAAACCCAG 1079
QY 155 AAGTTGAAGTACTTGGTGGAGAACGATTTGAAACCGGTTTACACTCCATCGACATCTCT 214
DB 1080 AAGTTGAAGTACTTGGTGGAGAACGATTTGAAACCGGTTTACACTCCATCGACATCTCT 1139
QY 215 TGTCTTGAACACAGTTTCTGTCTAGCGAGTTCTGTCACAGTGTCTGGTTCGTTCTCGAC 274
DB 1140 TGTCTTGAACACAGTTTCTGTCTAGCGAGTTCTGTCACAGTGTCTGGTTCGTTCTCGAC 1199
QY 275 TAGTTGAACATCATCTGGGGTATCTTGGTCCATCTCAATGGATTCATCTCGGGTCAAA 334
DB 1200 TAGTTGAACATCATCTGGGGTATCTTGTTCATCTCAATGGATTCATCTCGGGTCAAA 1259
QY 335 TTGACAGATTGATCAACAGAGATCGAAGAGTTCCGACGAAACGAGCCATCTCTAGAT 394
DB 1260 TTGACAGATTGATCAACAGAGATCGAAGAGTTCCGACGAAACGAGCCATCTCTAGAT 1319
QY 395 TGGAGAGATTGAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGATGGAGCCG 454
DB 1320 TGGAGAGATTGAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGATGGAGCCG 1379
QY 455 ATCTCACTAACCCAGCTCTCCGCGAGGAAATGCGATTCATTTCAACGACATGAACGCG 514
DB 1380 ATCTCACTAACCCAGCTCTCCGCGAGGAAATGCGATTCATTTCAACGACATGAACGCG 1439
QY 515 CTTTGACACAGCTATCCCATTTGTTGCGAGTCCAGAACTCAAGTTCTCTCTTGTGCG 574
DB 1440 CTTTGACACAGCTATCCCATTTGTTGCGAGTCCAGAACTCAAGTTCTCTCTTGTGCG 1499
QY 575 TGTACGTTCAACAGCTAATCTTTCACTTACGCTGCTTGAAGCTTTAGCGTTTGGCG 634
DB 1500 TGTACGTTCAACAGCTAATCTTTCACTTACGCTGCTTGAAGCTTTAGCGTTTGGCG 1559
QY 635 AAAGGTGGGATTCGATGCTGCAACCATCAATAGCGCTTACAAAGCATCTTACCTAGGCTGA 694
DB 1560 AAAGGTGGGATTCGATGCTGCAACCATCAATAGCGCTTACAAAGCATCTTACCTAGGCTGA 1619

QY 695 TTGGAACCTACACCGACCGCTGTTGTTGTAACAACCTGCTTGGACGTTCTGGG 754
DB 1620 TTGGAACCTACACCGACCGCTGTTGTTGTAACAACCTGCTTGGACGTTCTGGG 1679
QY 755 GTCTGATTTCTAGAGATTGATTAATCAACAGTTCCAGAGAGATTACCTCTCAG 814
DB 1680 GTCTGATTTCTAGAGATTGATTAATCAACAGTTCCAGAGAGATTACCTCTCAG 1739
QY 815 TTTTGACATTTGTTCTCTCTCCCGAAGTATGACTCCAACTCACTTACCTTCCGTACAG 874
DB 1740 TTTTGACATTTGTTCTCTCTCCCGAAGTATGACTCCAACTCACTTACCTTCCGTACAG 1799
QY 875 TGTCCCACTTACCAAGAAATCTAATCAACCCAGTTCTTGAGACTTGCAGCGTACT 934
DB 1800 TGTCCCACTTACCAAGAAATCTAATCAACCCAGTTCTTGAGACTTGCAGCGTACT 1859
QY 935 TCCGTGTTCTGCCAAGGTATGGAAGGCTCCATCAGAGGCCCACTTGATGAGCATCT 994
DB 1860 TCCGTGTTCTGCCAAGGTATGGAAGGCTCCATCAGAGGCCCACTTGATGAGCATCT 1919
QY 995 TGAACAGCATTAATCTATCAACCGATGCTCAAGAGAGATTAATCTGTTGAGACCC 1054
DB 1920 TGAACAGCATTAATCTATCAACCGATGCTCAAGAGAGATTAATCTGTTGAGACCC 1979
QY 1055 AGATCATGCGCTCTCAGTTGATTCAGCGGGCCGAGTTTACTTCTCTATGAA 1114
DB 1980 AGATCATGCGCTCTCAGTTGATTCAGCGGGCCGAGTTTACTTCTCTATGAA 2039
QY 1115 CTATGGGAACCGCGCTTCCACAAACAGTATCTGTTCTCAACTGATGATGATCTTACA 1174
DB 2040 CTATGGGAACCGCGCTTCCACAAACAGTATCTGTTCTCAACTGATGATGATCTTACA 2099
QY 1175 GAACCTTGTCTTCCACCTTGAACAGAGACCTTCAATATGATGATCAACACAGAAC 1234
DB 2100 GAACCTTGTCTTCCACCTTGAACAGAGACCTTCAATATGATGATCAACACAGAAC 2159
QY 1235 TTTTCGTTCTTGAACGAAACAGATTGCTCTATGAAACCTTCTTCACTTGCATCCGCTG 1294
DB 2160 TTTTCGTTCTTGAACGAAACAGATTGCTCTATGAAACCTTCTTCACTTGCATCCGCTG 2219
QY 1295 TTTTCAAGAAAGGGGAAACCGTTGATCTTGGAGGAAATCCCAACAGAAACAATG 1354
DB 2220 TTTTCAAGAAAGGGGAAACCGTTGATCTTGGAGGAAATCCCAACAGAAACAATG 2279
QY 1355 TGCCACCGAGCAAGATTTCTCCACAGTTGACCAAGTTCATGTTCCGTTCCGAT 1414
DB 2280 TGCCACCGAGCAAGATTTCTCCACAGTTGACCAAGTTCATGTTCCGTTCCGAT 2339
QY 1415 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATGATG 1474
DB 2340 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATGATG 2399
QY 1475 CTGAGTTCAAAATATCATTTCTTCTTCAAAATCCCAATTCGCAAGTGA 1534
DB 2400 CTGAGTTCAAAATATCATTTCTTCTTCAAAATCCCAATTCGCAAGTGA 2459
QY 1535 CTAACCTTGAATCTGAACTTCTGTCGTAAGAACAGGCTTCAAGAGAGTATTC 1594
DB 2460 CTAACCTTGAATCTGAACTTCTGTCGTAAGAACAGGCTTCAAGAGAGTATTC 2519
QY 1595 TTAGAAGAACTTCTCTGCGCAAGTATGACACCTTCAGAGTTTAACTCACTGACCACTTT 1654
DB 2520 TTAGAAGAACTTCTCTGCGCAAGTATGACACCTTCAGAGTTTAACTCACTGACCACTTT 2579
QY 1655 CTCAAGATATCGTGCAGATGTTGATGAGATCAACCTTAACCTGCAATTTCCAGACT 1714
DB 2580 CTCAAGATATCGTGCAGATGTTGATGAGATCAACCTTAACCTGCAATTTCCAGACT 2639
QY 1715 CCATGACGGAAGGCTATCAATCAAGGTTAACTTCTCCGCAACCATGTCAGCGGACAGA 1774
DB 2640 CCATGACGGAAGGCTATCAATCAAGGTTAACTTCTCCGCAACCATGTCAGCGGACAGA 2699

Db	961	GATCATGCGCTCTTCCAGTTGGATTCAAGGGGCCGAGTTTACCTTCTCTATGGAAC	1020
Qy	1116	TATGGAAAGCGCGCTCCACAAACAAGTATCGTTCTCAACTAGTCAGGGTGTCTACAG	1175
Db	1021	TATGGAAAGCGCGCTCCACAAACAAGTATCGTTCTCAACTAGTCAGGGTGTCTACAG	1080
Qy	1176	AACCTTGTCTTCCACTTTGTACAGAAACCCTTCATATCGGTATCAACAACGCAACT	1235
Db	1081	AACCTTGTCTTCCACTTTGTACAGAAACCCTTCATATCGGTATCAACAACGCAACT	1140
Qy	1236	TTCCGCTCTTGAAGGAAACAGAGTTCCGCTATAGAAACCTTCTTCACTTGGCATCCGCTGT	1295
Db	1141	TTCCGCTCTTGAAGGAAACAGAGTTCCGCTATAGAAACCTTCTTCACTTGGCATCCGCTGT	1200
Qy	1296	TTACAGAAAGAGCGGAACCGTTGATTCCTTTGGAAGAAATCCACACAGAAACAATGT	1355
Db	1201	TTACAGAAAGAGCGGAACCGTTGATTCCTTTGGAAGAAATCCACACAGAAACAATGT	1260
Qy	1356	GCCACCAAGCAGAGGATTTCTCCACAGGTTGAGCCACGTTGCATGTTCCGTTCCGATT	1415
Db	1261	GCCACCAAGCAGAGGATTTCTCCACAGGTTGAGCCACGTTGCATGTTCCGTTCCGATT	1320
Qy	1416	CAGCAACAGTTCGCTGAGCATCAACAGAGCTCCATGTTCTCATGAGTATCATCGTAGGC	1475
Db	1321	CAGCAACAGTTCGCTGAGCATCAACAGAGCTCCATGTTCTCATGAGTATCATCGTAGGC	1380
Qy	1476	TGAGTTCAACATATCATTTCTTCTCTCTCAATACCCAAATGCCATTGACCAAGTCTAC	1535
Db	1381	TGAGTTCAACATATCATTTCTTCTCTCTCAATACCCAAATGCCATTGACCAAGTCTAC	1440
Qy	1536	TAACTTTGATCTGGAACCTTCTGTGTGTGAAAGAACAGGCTTCAACAGAGGTGATATTCT	1595
Db	1441	TAACTTTGATCTGGAACCTTCTGTGTGTGAAAGAACAGGCTTCAACAGAGGTGATATTCT	1500
Qy	1596	TAGAAAGAACTTCTCTTGCCAGATTAGAACCCCTCAGAGTTAAATCATCTGCACCACTTTC	1655
Db	1501	TAGAAAGAACTTCTCTTGCCAGATTAGAACCCCTCAGAGTTAAATCATCTGCACCACTTTC	1560
Qy	1656	TCAAAAGATATCGTGTCAAGAGTTCCGTTAGCATCTACACTTAAGTTGCCAACCTTC	1715
Db	1561	TCAAAAGATATCGTGTCAAGAGTTCCGTTAGCATCTACACTTAAGTTGCCAACCTTC	1620
Qy	1716	CATCGACGGAAGGCTTATCAATCAAGGGTAACTTCTCCGCAACCATGTCAAGCGGACGAA	1775
Db	1621	CATCGACGGAAGGCTTATCAATCAAGGGTAACTTCTCCGCAACCATGTCAAGCGGACGAA	1680
Qy	1776	CTTGCAATCCGGCAGCTTCAAGAACGCTGGTTTTCACTACTCTCTTCAACTTCTCTAACGG	1835
Db	1681	CTTGCAATCCGGCAGCTTCAAGAACGCTGGTTTTCACTACTCTCTTCAACTTCTCTAACGG	1740
Qy	1836	ATCAAGCGCTTTTCAACCTTTAGCGCTCATGTGTTCATTTCTGAGCAATGAAGTATCAATGA	1895
Db	1741	ATCAAGCGCTTTTCAACCTTTAGCGCTCATGTGTTCATTTCTGAGCAATGAAGTATCAATGA	1800
Qy	1896	CCGATATTGATTTGTGCTCGCGGAAGTTACCTTCGAGGCTGAGTACT 1942	
Db	1801	CCGATATTGATTTGTGCTCGCGGAAGTTACCTTCGAGGCTGAGTACT 1847	
RESULT 15			
AAD06308			
ID	AAD06308 standard; DNA; 1851 BP.		
XX	AAD06308;		
AC			
XX	10-AUG-2001 (first entry)		
DT			
XX	Insecticidal CryIAb toxin DNA of Bt kurstaki expression cassette.		
DE			
XX			
KW	Transgenic maize; expression cassette; 35S promoter; NOS		
KW	alcohol dehydrogenase intron; neopline synthetase; NOS terminator;		
KW	crystal IAb; CryIAb toxin; foodstuffs preparation; ds.		

XX	OS	Bacillus thuringiensis.
XX	Key	Location/Qualifiers
XX	Key	2..1849
XX	Key	/*tag= a
XX	Key	/product= "insecticidal CryIAb toxin"
XX	US6222104-B1.	
XX	24-APR-2001.	
XX	13-APR-1999;	99US-0291238.
XX	09-NOV-1994;	94US-0336627.
XX	22-AUG-1996;	96US-0716836.
XX	14-MAR-1997;	97US-0818573.
XX	13-MAR-1998;	98US-0042426.
XX	(NOVS) NOVARTIS AG.	
XX	Mettler ID, Krier M, Mies D;	
XX	WPI; 2001-327266/34.	
XX	P-PSDB; AAE02360.	
XX	Novel transgenic maize seed for hybrid maize plant production,	
XX	comprising expression cassette linked operably with CMV 35S promoter,	
XX	alcohol dehydrogenase intron, insecticidal CryIAb toxin gene or NOS	
XX	terminator -	
XX	Claim 1; Column 19-22; 24pp; English.	
XX	The present invention relates to transgenic maize seed for hybrid maize	
XX	plant production, comprising an expression cassette linked operably with	
XX	constitutive Cauliflower mosaic virus (CaMV) 35S promoter, an alcohol	
XX	dehydrogenase intron, a DNA encoding an insecticidal	
XX	Bacillus thuringiensis (Bt) CryIAb toxin and a nopaline synthetase (NOS)	
XX	terminator. The transgenic maize seed is used in maize cultivation	
XX	methods for propagating hybrid maize seeds and for growing hybrid maize	
XX	plants. The maize is also used in foodstuffs preparation for animal or	
XX	human consumption. The inbred maize line NP948 of the invention has	
XX	reduced level of fungal toxins, hence suitable for foodstuffs	
XX	preparation. Yield is high. Plant health is improved due to reduced	
XX	stalk rot. Grain test weight is high and the rate of grain dry down is	
XX	reduced. The present sequence is insecticidal crystal IAb (CryIAb) toxin	
XX	DNA of Bt kurstaki expression cassette.	
XX	Sequence 1851 BP; 478 A; 504 C; 394 G; 475 T; 0 other;	
XX	Query Match 66.2%; Score 1845.4; DB 22; Length 1851;	
XX	Best Local Similarity 99.9%; Pred. No. 0;	
XX	Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0	
XX	96 CATGACAAACCAACCAACATTAAGATGCTTGCATPACAACTGTTGAGTAAACCAAA 155	
XX	1 CATGACAAACCAACCAACATTAAGATGCTTGCATPACAACTGTTGAGTAAACCAAA 60	
XX	156 AGTTAAGACTTGGTGGAGAAACGATTGAACCGATTACATCCATGACATCTCTT 215	
XX	61 AGTTAAGACTTGGTGGAGAAACGATTGAACCGATTACATCCATGACATCTCTT 120	
XX	216 GTCTTGAACACAGTTTGTGCTCAGCGAGTTGTGTCAGAGTGTGGTTCGTTCCGACT 275	
XX	121 GTCTTGAACACAGTTTGTGCTCAGCGAGTTGTGTCAGAGTGTGGTTCGTTCCGACT 180	
XX	276 AGTTGACATCATCTGGGGTATCTTTTGTGCTCAATGGAATGCAATTCGTGTGCAAA 335	
XX	181 AGTTGACATCATCTGGGGTATCTTTTGTGCTCAATGGAATGCAATTCGTGTGCAAA 240	
XX	336 TGAGGAGTTGATCAACAGAGGATGGAAGATTTCGACAGGAACAGAGCATCTTAGTT 395	
XX	241 TGAGGAGTTGATCAACAGAGGATGGAAGATTTCGACAGGAACAGAGCATCTTAGTT 300	

OY	396	GGAAGGATTGAGCAATCTCTACCAAAATCTATGCGAGAAGCTTCGAGAAGTGGGAAAGCCGA	455
Db	301	GGAGGATTGAGCAATCTCTACCAAAATCTATGCGAGAAGCTTCGAGAAGTGGGAAAGCCGA	360
OY	456	TCCTACTAACCCAGACTCTCCGCGAGGAATGCGATTCAATTCAACGACATGAACAGCGC	515
Db	361	TCCTACTAACCCAGACTCTCCGCGAGGAATGCGATTCAATTCAACGACATGAACAGCGC	420
OY	516	CTTBAACCAAGACTATGCCATTGTTCCGAGTCCCAAACTTACCAGTTCTCTCTGTCCTGT	575
Db	421	CTTBAACCAAGACTATGCCATTGTTCCGAGTCCCAAACTTACCAGTTCTCTCTGTCCTGT	480
OY	576	GTAAGCTTCAAGACACTAATCTTCAACCTCAGCGTCTTTCAGACGTTAGCGTGTGAGGCA	635
Db	481	GTAAGCTTCAAGACACTAATCTTCAACCTCAGCGTCTTTCAGACGTTAGCGTGTGAGGCA	540
OY	636	AAGGTGGGGATTGCAATGCTGTCACCACTCATATGCCGTTTACAACAAGCTTACTAGCGTAT	695
Db	541	AAGGTGGGGATTGCAATGCTGTCACCACTCATATGCCGTTTACAACAAGCTTACTAGCGTAT	600
OY	696	TGGAAACTACACCGAACCAACGCTGTTTCGTTGGTATACAACATCGCTTGGAGCGGTCTGAGG	755
Db	601	TGGAAACTACACCGAACCAACGCTGTTTCGTTGGTATACAACATCGCTTGGAGCGGTCTGAGG	660
OY	756	TCCTGATTCTAGAGATTGGATTAGATACAAACAGTTCAGAGAGAATTTGACCTCAGAGT	815
Db	661	TCCTGATTCTAGAGATTGGATTAGATACAAACAGTTCAGAGAGAATTTGACCTCAGAGT	720
OY	816	TTTGGACATTGTGTCTCTTCTCCGGAATATGACTCCGAAGCTTACCTATCCGTACAGT	875
Db	721	TTTGGACATTGTGTCTCTCTCCGGAATATGACTCCGAAGCTTACCTATCCGTACAGT	780
OY	876	GTCCCAACTTACAGAGAAATCTATATCTAACCCAGTTCCTTAGAAGCTTCGACGGTAGCTT	935
Db	781	GTCCCAACTTACAGAGAAATCTATATCTAACCCAGTTCCTTAGAAGCTTCGACGGTAGCTT	840
OY	936	CCGTGGTCTGCCCCAAGGTATCGAAGGCTCATAGAGGCCCAACCTTGATGACATCTT	995
Db	841	CCGTGGTCTGCCCCAAGGTATCGAAGGCTCATAGAGGCCCAACCTTGATGACATCTT	900
OY	996	GAAACAGCACTACTATCTATCTACACCGATGCTCACAAGAGAGATTAATCTGCTGTGACACCA	1055
Db	901	GAAACAGCACTACTATCTATCTACACCGATGCTCACAAGAGAGATTAATCTGCTGTGACACCA	960
OY	1056	GATCATGGCCTCTCCAGTTGGATTCAAGCGGAGCCGAGATTACCTTCTCTCTATGGAAC	1115
Db	961	GATCATGGCCTCTCCAGTTGGATTCAAGCGGAGCCGAGATTACCTTCTCTCTATGGAAC	1020
OY	1116	TATGAGGAAACGCGCTCTCACAACAACGTAATGTTGCTCAACTAGTCAAGGTGTCTACAG	1175
Db	1021	TATGAGGAAACGCGCTCTCACAACAACGTAATGTTGCTCAACTAGTCAAGGTGTCTACAG	1080
OY	1176	AACCTTGCTTTCACCTTGTAACAGAAAGCCTTCAATTCGTAATCAACAACAGCAACT	1235
Db	1081	AACCTTGCTTTCACCTTGTAACAGAAAGCCTTCAATTCGTAATCAACAACAGCAACT	1140
OY	1236	TTCCGTTCTTGAACGAGACAGAGTTCCGCTATGGAACCTTCTTCAACTTGCATCCGCTGT	1295
Db	1141	TTCCGTTCTTGAACGAGACAGAGTTCCGCTATGGAACCTTCTTCAACTTGCATCCGCTGT	1200
OY	1296	TTACAGAAAGAGCGGACCGTTGATTCCTTGGACGAATTCACACAGAACCAACAATGT	1355
Db	1201	TTACAGAAAGAGCGGACCGTTGATTCCTTGGACGAATTCACACAGAACCAACAATGT	1260
OY	1356	GCCACCCAGGCAAGGATTCCTCCACAGGTTGAGCCACGTGTCAATGTTCCGTTCCGAGTT	1415
Db	1261	GCCACCCAGGCAAGGATTCCTCCACAGGTTGAGCCACGTGTCAATGTTCCGTTCCGAGTT	1320
OY	1416	CAGCAACAGTTTCCGTGAGCATATCAGAGCTCTATGTTCTCATGGAATTCATCGTAAGTC	1475
Db	1321	CAGCAACAGTTTCCGTGAGCATATCAGAGCTCTATGTTCTCATGGAATTCATCGTAAGTC	1380

QY	1476	TGAGTTCAACAATATCATCTCTCTCTCAATATACCCAATCCCATTTGACCAAGTCTAC	1535
Db	1381	TGAGTTCAACAATATCATCTCTCTCTCTCAATATACCCAATCCCATTTGACCAAGTCTAC	1440
QY	1536	TAACTCTTGATCTTGAACTTCTGTGCTGTAAGACACAGGCTTTCACAGAGGTGATATTCT	1595
Db	1441	TAACTCTTGATCTTGAACTTCTGTGCTGTAAGACACAGGCTTTCACAGAGGTGATATTCT	1500
QY	1596	TAGAAGAACTTCTTCCTGCGCAGATTACACCTCTCAGAGTTAACTCATCTGCACACATTTCT	1655
Db	1501	TAGAAGAACTTCTTCCTGCGCAGATTACACCTCTCAGAGTTAACTCATCTGCACACATTTCT	1560
QY	1656	TCAAAGATATCGTGTCAAGATTGGTTACGCAATCACAATACTTGGAAATTTCCACACCTC	1715
Db	1661	TCAAAGATATCGTGTCAAGATTGGTTACGCAATCACAATACTTGGAAATTTCCACACCTC	1620
QY	1716	CATGACGGAAGGCTTATCATATCAGGGTAATTTCTCCGCAACCATATGTCACAGGGCAGCA	1775
Db	1621	CATGACGGAAGGCTTATCATATCAGGGTAATTTCTCCGCAACCATATGTCACAGGGCAGCA	1680
QY	1776	CTTGCAATCCGGCAGCTTCAGAACCGTCGGATTTCACTACTCTTTCAACTCTCTTAAACGG	1835
Db	1681	CTTGCAATCCGGCAGCTTCAGAACCGTCGGATTTCACTACTCTTTCAACTCTCTTAAACGG	1740
QY	1836	ATCAAGCGTTTTCACCCCTTAGCGCTCATGTGTTCATTTCTGGCAATGAAGTGTACATTGA	1895
Db	1741	ATCAAGCGTTTTCACCCCTTAGCGCTCATGTGTTCATTTCTGGCAATGAAGTGTACATTGA	1800
QY	1896	CCGATATTGATTTGTGCTGCTGCCGAAGTAACTTCTGAGAGCTGAGTAAGT 1942	
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Search completed: October 21, 2003, 09:58:40
Job time : 713 secs

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 Db 1080 AAGTTGAAGTACTTGTTGGAGAACGATTTGAACCGGTTTACACTCCCATCGACATCTCT 1139
 Oy 215 TGTCTTGACACAGTTTCTGCTCAGCGAGTTCTGTCCAGAGTGTGGGTTCTGTTCCGAC 274
 Db 1140 TGTCTTGACACAGTTTCTGCTCAGCGAGTTCTGTCCAGAGTGTGGGTTCTGTTCCGAC 1199
 Oy 275 TAGTTGACATCATCTGGGGGTATCTTTGGTCCATCTCAATGGGATGCAATTTCTGTGGCAA 334
 Db 1200 TAGTTGACATCATCTGGGGGTATCTTTGGTCCATCTCAATGGGATGCAATTTCTGTGGCAA 1259
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 Db 2220 TTTTACAGAAAGCGGAAACGTTGATTTCTTGAACGAAATCCACACAGAACAAATG 2279
 Oy 1355 TGCCACCCAGGCAAGATTTCCCAAGTTGAGCCAGTGTCCATGTTCCGTTCCGGAT 1414
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 Oy 1415 TCAGCAACAGTTCGCTGAGATCAATCAGAGCTCTATGTTCTCATGATTCATGATG 1474
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 Db 2520 TTGAGAAACTTCTCTGCGCAGATTAGACACCTCAGAGTTTACATCACTGACCACTT 2579
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 Db 2760 GATCAAGCTTTTACACCTTAGCGCTCATGTTCTTCTTGGGAATGAATGATG 2819
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 Db 2820 ACCGATTTGATTTGTGCTCCGAAATACCTTCAGAGCTGATGATGATTCATGTC 2879
 Oy 1955 T 1955
 Db 2880 T 2880

RESULT 2
 US-09-291-238-9
 ; Sequence 9, Application US/09291238
 ; Patent No. 6222104
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
 ; TITLE OF INVENTION: DNA Construct Containing Bacillus
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6222104artis Corporation
 ; STREET: 564 Morris Avenue
 ; CITY: Summit
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07901
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7378 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Complete sequence of pZ01502
US-09-291-238-9

Query March 66.3%; Score 1848.2; DB 3; Length 7378;

Best Local Similarity 99.6%; Pred. No. 0; Mismatches 8; Indels 0; Gaps 0;

March 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 95 CCATGACACAGCCCAACATCAAGATGATTCATACACTGCTTGAGTAACCCAG 154
DB 1020 CCATGACACACACCCCAACATCAAGATGATTCATACACTGCTTGAGTAACCCAG 1079
QY 155 AAGTTGAAGTACTTGTTGAGAGAACGATTTGAAACCGGTTACACTCTCCATCGACATCTCT 214
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QY 215 TGTCTTGACACAGTTTCTGCTCAGCGAGTTGCTGCGAGGTCGTTGCTTCTCGAGC 274
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DB 1500 TGTAGCTTCAAGCAGCTATCTTCACTCAGCGCTTCCAGAGCTTACGCTTTAGGCG 1559
QY 635 AAAAGTGGGAGTTTCAGTGTGCAACCATCAATAGCGCTTCAACGACCTTACTAGAGCTGA 694
DB 1560 AAAAGTGGGAGTTTCAGTGTGCAACCATCAATAGCGCTTCAACGACCTTACTAGAGCTGA 1619
QY 695 TTGGAACCTACACGACGCTGTTCTGGTACAACTGAGCTTGGAGCGTGTGCG 754

DB 1620 TTGGAACCTACACGACGCTGTTCTGGTACAACTGAGCTTGGAGCGTGTGCG 1679
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QY 815 TTTTGGACATTTGCTCTCTTCCGCACTATGATCTCAGAACCTTACCTTCTGACAG 874
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DB 1800 TGTCCCACTTACAGAGAAATCTATCTAACCCAGTTCTTGAAGTCTGAGAGCT 1859
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DB 2100 GAACTTGTCTTCCACTTGTACAGAAAGCCCTTCAATATCGGTATCAACACGACAC 2159
QY 1235 TTTCCGTTCTTGAAGGAAAGAGTTGGCTATGGAACCTCTTCACTGTCATCGCGTG 1294
DB 2160 TTTCCGTTCTTGAAGGAAAGAGTTGGCTATGGAACCTCTTCACTGTCATCGCGTG 2219
QY 1295 TTTACAGAAAGAGCGGAACCGTTGATTCCTTGAAGAAATCCCAACAGAAACATG 1354
DB 2220 TTTACAGAAAGAGCGGAACCGTTGATTCCTTGAAGAAATCCCAACAGAAACATG 2279
QY 1355 TGCCACCGAGCAAGATTTCTCCACAGGTTGAGCCACGTCATGTTCCGTTCCGAT 1414
DB 2280 TGCCACCGAGCAAGATTTCTCCACAGGTTGAGCCACGTCATGTTCCGTTCCGAT 2339
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QY 1475 CTGAGTTCAACAAATATCTCTCTCTCAATACCAACCAATCCATTGCAAGTCTA 1534
DB 2400 CTGAGTTCAACAAATATCTCTCTCTCTCAATACCAACCAATCCATTGCAAGTCTA 2459
QY 1535 CTAACTTTGATCTGGAACCTTCTGTCGTGAAGAGCAAGCTTCAACAGAGAGTATTC 1594
DB 2460 CTAACTTTGATCTGGAACCTTCTGTCGTGAAGAGCAAGCTTCAACAGAGAGTATTC 2519
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DB 2520 TTAAGAAGCTTCTCTGCGGAGATTTAGCACTCAGAGTTTACATCACTGACACACTTT 2579
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DB 2580 CTCAAGATATCTGTGAGATTCGTTACGATCTACCACTTGTGCAATTCACACCT 2639
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DB 2640 CCAATGACGGAAGGCTATCAATCAGGTTAACTTCTCGCAACCATGTCAGAGCGGACGA 2699
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Db 2700 ACTTGCAATCCGCGACCTTCAGAAACCGTGGTTTCACTCTTCACTTCTCTACG 2759
Qy 1835 GATCAAGCGTTTTCACCTTAGCGCTCATGTGTTCAATTCTGGCAATGAGTATACATG 1894
Db 2760 GATCAAGCGTTTTCACCTTAGCGCTCATGTGTTCAATTCTGGCAATGAGTATACATG 2819
Qy 1895 ACCGTTATGAGTTGTGCTCCCGAAGTTACCTTCGAGGCTGAGTACTGAGAAATTATCGC 1954
Db 2820 ACCGTTATGAGTTGTGCTCCCGAAGTTACCTTCGAGGCTGAGTACTGAGAAATTATCGC 2879
Qy 1955 T 1955
Db 2880 T 2880

RESULT 3
US-09-330-760-9
Sequence 9, Application US/09330760
Patent No. 6229075
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7378 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Complete sequence of pZO1502
US-09-330-760-9

Query Match 66.3%; Score 1848.2; DB 3; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 95 CCATGAGCAACAACCAACATCAACGATTCATCACTGCTTGAGTAAACCGAG 154
Db 1020 CCATGAGCAACAACCAACATCAACGATTCATCACTGCTTGAGTAAACCGAG 1079
Qy 155 AAGTTGAAGTACTTGATGAGAAAGCATTTGAACCGGTTACACTCCATCGACATCTCT 214
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Qy 215 TGTCTTGAACAAGATTCTCTCAGAGAGTTGCTGCCAGGTGCTGGTGTCTCGGAC 274
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Db 1380 ATCTACTAACCCAGCTCTCCGGAGGAATGGGTATTCAATTCAAGACATGAACAGCG 1439
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Qy 1235 TTTTCGTTCTTGAAGGAAAGAGTTGCTATGAAACCTCTTCTACTTGCATTCGCTG 1294
Db 2160 TTTTCGTTCTTGAAGGAAAGAGTTGCTATGAAACCTCTTCTACTTGCATTCGCTG 2219

QY	1295	TTTACAGAAAGAGGGGAAACCGTTGATTCCTTGACGAAATCCCAACACAGAAACAATG	1354
Db	2220	TTTACAGAAAGAGGGGAAACCGTTGATTCCTTGACGAAATCCCAACACAGAAACAATG	2279
QY	1355	TGCCACCAGGCGAAGATTCCTCCACAGGTTAGCCAGTGTCCATGTTCCGTTCCGAT	1414
Db	2280	TGCCACCAGGCGAAGATTCCTCCACAGGTTAGCCAGTGTCCATGTTCCGTTCCGAT	2339
QY	1415	TCAGCAACAGTCCGTGAGCATCATCAGAGCTCCTAAGTTCTCAGTGGATTCATGTAAGT	1474
Db	2340	TCAGCAACAGTCCGTGAGCATCATCAGAGCTCCTAAGTTCTCAGTGGATTCATGTAAGT	2399
QY	1475	CTGAGTTCAACAATATCATCTTCCTTCCTTCAATACCCAAATCCCATTTGACCAAGTCTA	1534
Db	2400	CTGAGTTCAACAATATCATCTTCCTTCCTTCAATACCCAAATCCCATTTGACCAAGTCTA	2459
QY	1535	CTAACCTTGATCTGCGAACTTCCTGCGGAAAGACCAAGGCTTCACAGAGAGTAAATTC	1594
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Db	2520	TTAGAAGAACTTCCTGCGCGAGATTAGCAACCTCCAGAGTTAAGATCACTGCACCACTT	2579
QY	1655	CTCAAAGATATCGTGTACAGATTCTGTACGATCTACCAACAACTTGCAATTCACACCT	1714
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Db	2640	CCATCGACGGGAAGCCATCATCAGGGTACTCTCCGCAACCATATGCAACGGCGACGA	2699
QY	1775	ACTTGCAATCCGGGAGCTTCAGAAACCGTCGGTTCACTACTCTTCAACTCTCTAAG	1834
Db	2700	ACTTGCAATCCGGGAGCTTCAGAAACCGTCGGTTCACTACTCTTCAACTCTCTAAG	2759
QY	1835	GATCAAGGTTTTACCCCTTAGCGCTCATGTGTTCAATTCGCGCAATGAATGATCATG	1894
Db	2760	GATCAAGGTTTTACCCCTTAGCGCTCATGTGTTCAATTCGCGCAATGAATGATCATG	2819
QY	1895	ACCGTATTGATTTGTGCTGCCGGAAGTTACCTTCGAGGCTGAGTACTGAAATTAATGC	1954
Db	2820	ACCGTATTGATTTGTGCTGCCGGAAGTTACCTTCGAGGCTGAGTACTGAAATTAATGC	2879
QY	1955	T 1955	
Db	2880	T 2880	
RESULT 4			
US-09-328-473-9			
Sequence 9, Application US/09328473			
Patent No. 6232533			
GENERAL INFORMATION:			
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinnabaldi			
TITLE OF INVENTION: DNA Construct Containing Bacillus			
NUMBER OF SEQUENCES: 11			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: No. 6232533artis Corporation			
STREET: 564 Morris Avenue			
CITY: Summit			
STATE: New Jersey			
COUNTRY: USA			
ZIP: 07901			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patent Release #1.0, Version #1.25			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/328,473			
FILING DATE:			
CLASSIFICATION:			

Query Match	Best Local Similarity	Score	DB 3	Length	7378	
Matches 1853	Conservative	0	Mismatches	8	Indels	0
					Gaps	0
<p>Prior Application Data:</p> <p>Application Number: 09/042,426</p> <p>Filing Date: March 13, 1998</p> <p>Attorney/Agent Information:</p> <p>Name: Hoxie, Thomas</p> <p>Registration Number: 32,993</p> <p>Reference/Docket Number: 135/1</p> <p>Telecommunication Information:</p> <p>Telephone: (919) 541-8614</p> <p>Telefax: (919) 541-8689</p> <p>Information for SEQ ID NO: 9:</p> <p>Sequence Characteristics:</p> <p>Length: 7378 base pairs</p> <p>Type: nucleic acid</p> <p>Strandedness: double</p> <p>Topology: linear</p> <p>Molecule Type: DNA (genomic)</p> <p>Hypothetical: NO</p> <p>Anti-Sense: NO</p> <p>Immediate Source:</p> <p>Clone: Complete sequence of pZOL502</p> <p>US-09-328-473-9</p>						
Query	95	CCATGCAACAAACCCAAACATCAGCAATGCATTCATCAACACTGCTTGTAACCG	154			
Db	1020	CCATGCAACAAACCCAAACATCAGCAATGCATTCATCAACACTGCTTGTAACCG	1079			
Qy	155	AAGTTGAAGTACTTGTGTGAGAGACGATTGAAACCGGTACCTCCATGCAATCTCT	214			
Db	1080	AAGTTGAAGTACTTGTGTGAGAGACGATTGAAACCGGTACCTCCATGCAATCTCT	1139			
Qy	215	TGTCCTTGACACGATTTCTGCTGACGAGTTCGTCACGAGGCTGGGTTCTTCCGAC	274			
Db	1140	TGTCCTTGACACGATTTCTGCTGACGAGTTCGTCACGAGGCTGGGTTCTTCCGAC	1199			
Qy	275	TAGTTGACATCATCTGGGATTCCTTGGTCCATCTCAATGGAGTGCATCTCTGTGCAA	334			
Db	1200	TAGTTGACATCATCTGGGATTCCTTGGTCCATCTCAATGGAGTGCATCTCTGTGCAA	1258			
Qy	335	TTGAGCAGTTCATCAACGAGGATTCGAAAGTTCGCGAGAACGAGCCATCTCTAGT	394			
Db	1260	TTGAGCAGTTCATCAACGAGGATTCGAAAGTTCGCGAGAACGAGCCATCTCTAGT	1319			
Qy	395	TGGAAGATTGAGCAATCTCTACCAAACTCTATGAGAGAGCTTGAGAGTGGGAAGCG	454			
Db	1320	TGGAAGATTGAGCAATCTCTACCAAACTCTATGAGAGAGCTTGAGAGTGGGAAGCG	1379			
Qy	455	ATCTTAATCAACCCAGCTCTCCGCGAGGAATGCGTATTCAATTCAACGACATGAAACCG	514			
Db	1380	ATCTTAATCAACCCAGCTCTCCGCGAGGAATGCGTATTCAATTCAACGACATGAAACCG	1439			
Qy	515	CCTTGACACGATATCCCATTTGTTCGAGTCGAAATTAACCAAGTTCTCTCTTGTGCG	574			
Db	1440	CCTTGACACGATATCCCATTTGTTCGAGTCGAAATTAACCAAGTTCTCTCTTGTGCG	1499			
Qy	575	TGTAAGTTCAAGCAGCTATCTTCACTCAGCGTGTTCGAGCGTTAGCGTTTGGCG	634			
Db	1500	TGTAAGTTCAAGCAGCTATCTTCACTCAGCGTGTTCGAGCGTTAGCGTTTGGCG	1555			
Qy	635	AAAGTGGGGATTGATGTCGCAACCATATAGCCGTTAACAAGACTTCTAGCTGA	694			
Db	1560	AAAGTGGGGATTGATGTCGCAACCATATAGCCGTTAACAAGACTTCTAGCTGA	1615			
Qy	695	TTGAAATCAACCGACCGCTGTCTGTTGGTCAACAACACTGGCTGGAGCGTGTCTGGG	754			
Db	1620	TTGAAATCAACCGACCGCTGTCTGTTGGTCAACAACACTGGCTGGAGCGTGTCTGGG	1679			
Qy	755	GTCTGATTTCTAGATTTGATTTAGTTCACCGTTTACGAGAGAAATTGACCCCTCACAG	814			

Db 1680 GTCTGATCTTAGAGATTGATTTAGATACAAACAGTTCCAGAGAGAAATTCACCTCACAG 1739
Qy 815 TTTTGACATTTGTGTCTCTCTTCCGGAATGATGATCCAGAACTTACCTTACCGTACAG 874
Db 1740 TTTTGACATTTGTGTCTCTCTTCCGGAATGATGATCCAGAACTTACCTTACCGTACAG 1799
Qy 875 TGTCCCAACTTACAGAGAAATCTAATTAACCCAGTTCTTGAGAACTTGACGGTAGCT 934
Db 1800 TGTCCCAACTTACAGAGAAATCTAATTAACCCAGTTCTTGAGAACTTGACGGTAGCT 1859
Qy 935 TCCGTGTTCTGCGCCAGAGTATCGAAGGCTCATCAGGAGCCACACTGATGAGCAACT 994
Db 1860 TCCGTGTTCTGCGCCAGAGTATCGAAGGCTCATCAGGAGCCACACTGATGAGCAACT 1919
Qy 995 TGAACAGATTAATATCTACACAGGATGCTCAGAGAGAGATATTAATGCTGTGGACACC 1054
Db 1920 TGAACAGATTAATATCTACACAGGATGCTCAGAGAGAGATATTAATGCTGTGGACACC 1979
Qy 1055 AGATCATGGCTCTCCAGTTGAGATTGACGGGCGCCGAGTTTACCTTCTCTATGGAA 1114
Db 1980 AGATCATGGCTCTCCAGTTGAGATTGACGGGCGCCGAGTTTACCTTCTCTATGGAA 2039
Qy 1115 CTATGGGAAAAGCGCGCTCCACAAACGATGTTGCTCAACCTAGTTCAGGAGTGTCTACA 1174
Db 2040 CTATGGGAAAAGCGCGCTCCACAAACGATGTTGCTCAACCTAGTTCAGGAGTGTCTACA 2099
Qy 1175 GAACCTTGCTTCCACCTTGTACAGAAAGACCTTCAATATGCGATCAACAACAGCAAC 1234
Db 2100 GAACCTTGCTTCCACCTTGTACAGAAAGACCTTCAATATGCGATCAACAACAGCAAC 2159
Qy 1235 TTTCCGTTCTTGACGGAAACAGATTGGCTTATGAACTCTTCTAATCTGCTCATCCGCTG 1294
Db 2160 TTTCCGTTCTTGACGGAAACAGATTGGCTTATGAACTCTTCTAATCTGCTCATCCGCTG 2219
Qy 1295 TTTTACAGAAAGCGGAAACCGTTGATTCCTTGAAGAAATCCCAACAGAAACAAATG 1354
Db 2220 TTTTACAGAAAGCGGAAACCGTTGATTCCTTGAAGAAATCCCAACAGAAACAAATG 2279
Qy 1355 TGCCACCCAGGCAAGAGATTTCTCCACAGGTTGAGCCAGTGTCACTGTTCCGTTCCGAT 1414
Db 2280 TGCCACCCAGGCAAGAGATTTCTCCACAGGTTGAGCCAGTGTCACTGTTCCGTTCCGAT 2339
Qy 1415 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATCGTAGTG 1474
Db 2340 TCAGCAACAGTTCCGTGAGCATCATCAGAGCTCTATGTTCTCATGATTCATCGTAGTG 2399
Qy 1475 CTGAGTTCAACATATCATTTCTTCTCTCAAAATACCCAAATCCCATTTGACCAAGTCTA 1534
Db 2400 CTGAGTTCAACATATCATTTCTTCTCTCAAAATACCCAAATCCCATTTGACCAAGTCTA 2459
Qy 1535 CTAACTTGGATCTGGAACCTTCTGTCGTGAAGGACAGAGCTTCACAGAGGTTGATTTG 1594
Db 2460 CTAACTTGGATCTGGAACCTTCTGTCGTGAAGGACAGAGCTTCACAGAGGTTGATTTG 2519
Qy 1595 TTAGAAGAACTTCTCTGCGCAAGATTAGCACTCAGAGTTAATCATCTGCAACCACTT 1654
Db 2520 TTAGAAGAACTTCTCTGCGCAAGATTAGCACTCAGAGTTAATCATCTGCAACCACTT 2579
Qy 1655 CTCAAAAGATATGTTGTCAAGATTTGTTAGCATCTACCACTAATTTGAAATTCACACT 1714
Db 2580 CTCAAAAGATATGTTGTCAAGATTTGTTAGCATCTACCACTAATTTGAAATTCACACT 2639
Qy 1715 CCATGAGAGGAGGCTATCAATCAAGGTAATCTTCTCGCAACCAATGTCAGGCGACAGA 1774
Db 2640 CCATGAGAGGAGGCTATCAATCAAGGTAATCTTCTCGCAACCAATGTCAGGCGACAGA 2699
Qy 1775 ACTTGAATCCGGCAGCTTCAAGAACCGTCGTTTCACTACTCTTCAACCTTCTTAACG 1834
Db 2700 ACTTGAATCCGGCAGCTTCAAGAACCGTCGTTTCACTACTCTTCAACCTTCTTAACG 2759
Qy 1835 GATCAAGGTTTCAACCTTACGGCTCATGTTGAATTTGGAATGAAAGTTGATTTG 1894
Db 2760 GATCAAGGTTTCAACCTTACGGCTCATGTTGAATTTGGAATGAAAGTTGATTTG 2819

Qy 1895 ACCGTAATGAGTTTGTCCTGCGGAAGTATACCTTGAGGCTGAGTACTGAGAAATTCATGC 1954
Db 2820 ACCGTAATGAGTTTGTCCTGCGGAAGTATACCTTGAGGCTGAGTACTGAGAAATTCATGC 2879
Qy 1955 T 1955
Db 2880 T 2880

RESULT 5
US-09-330-737-9
Sequence 9, Application US/09330737
Patent No. 6232534
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6232534artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330.737
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7378 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Complete sequence of pZ01502
US-09-330-737-9

Query Match 66.3%; Score 1848.2; DB 3; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 95 CCATGAGCAACCAACCAACATCAAGATGCATTCATACAACTGCTTGAATTAACCGAG 154
Db 1020 CCATGAGCAACCAACCAACATCAAGATGCATTCATACAACTGCTTGAATTAACCGAG 1079
Qy 155 AAGTTGAAGTACTTGTTGAGAGGATTTGAACCGTTTACAGTCCATCGACATCTCT 214
Db 1080 AAGTTGAAGTACTTGTTGAGAGGATTTGAACCGTTTACAGTCCATCGACATCTCT 1139
Qy 215 TGTCTTGACACAGTTTCTGCTCAGCGAGTTGTTGTCGAGGAGTGTGGTTGTTCTCGAGC 274
Db 1140 TGTCTTGACACAGTTTCTGCTCAGCGAGTTGTTGTCGAGGAGTGTGGTTGTTCTCGAGC 1199

QY 275 TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGAGATGCAATTCCTGTGCAAA 334
 DB 1200 TAGTTGACATCATCTGGGGTATCTTTGGTCCATCTCAATGGAGATGCAATTCCTGTGCAAA 1259
 QY 335 TTGAGCACTTATCAACGAGAGATCGAAGAGTTGCGCAGAGAACGAGCCATCTCTAGT 394
 DB 1260 TTGAGCACTTATCAACGAGAGATCGAAGAGTTGCGCAGAGAACGAGCCATCTCTAGT 1319
 QY 395 TGAAGAGTTGAGCAATCTACCAAAATCTATGAGAGAGCTTGAGAGTGGAGAGCG 454
 DB 1320 TGAAGAGTTGAGCAATCTACCAAAATCTATGAGAGAGCTTGAGAGTGGAGAGCG 1379
 QY 455 ATCTACTAACCCAGCTCTCCGCGAGAAATGCGTATTCATTCAGAGATGAACAGCG 514
 DB 1380 ATCTACTAACCCAGCTCTCCGCGAGAAATGCGTATTCATTCAGAGATGAACAGCG 1439
 QY 515 CCTTGACCAAGCTATCCCATTTGTTGCGAGTCCAGAAATACCAAGTTCTCTCTGTCG 574
 DB 1440 CCTTGACCAAGCTATCCCATTTGTTGCGAGTCCAGAAATACCAAGTTCTCTCTGTCG 1499
 QY 575 TGTACGTTCAAGCACTATCTTCACCTCAGCGTCTTGAGAGCTTGAGAGCTTGAGAG 634
 DB 1500 TGTACGTTCAAGCACTATCTTCACCTCAGCGTCTTGAGAGCTTGAGAGCTTGAGAG 1559
 QY 635 AAAGTGGGGATTCGATCTGCAACCATCAATAGCGTTTACAGAGCCTTACTAGGCTGA 694
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 QY 695 TTGAGAAATACACCGACAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 754
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 DB 1680 GTCTGATTTAGAGATTTGATTTGATTTAGATTAACCAACAGTTGAGAGAAATTTGAGAG 1739
 QY 815 TTTTGGACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 874
 DB 1740 TTTTGGACATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1799
 QY 875 TGTCCCACTTACCGAGAGAAATCTATCTAACCCAGTTCTTGAGAAATTTGAGAGCTTCA 934
 DB 1800 TGTCCCACTTACCGAGAGAAATCTATCTAACCCAGTTCTTGAGAAATTTGAGAGCTTCA 1859
 QY 935 TCCGTGTTGTCGCGCAAGGATCGAAGGCTCCATGAGAGAGCCCACTTATGATGACATCT 994
 DB 1860 TCCGTGTTGTCGCGCAAGGATCGAAGGCTCCATGAGAGAGCCCACTTATGATGACATCT 1919
 QY 995 TGAACAGATTAATCTATCTACACCGATGCTCAGAGAGAGATTTAATGTTGTTGAGACAC 1054
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 QY 1055 AGATATAGGCTCTCAGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 1114
 DB 1980 AGATATAGGCTCTCAGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 2039
 QY 1115 CTATGGAAGAGCGCGCTCCACAACAGTATGTTGCTCACTAGAGTCAAGGTTGTTCA 1174
 DB 2040 CTATGGAAGAGCGCGCTCCACAACAGTATGTTGCTCACTAGAGTCAAGGTTGTTCA 2099
 QY 1175 GAACCTTGTCTTCACTTTGTAAGAGAGCCCTTCAATGCGTATCAACCAACAGCAAC 1234
 DB 2100 GAACCTTGTCTTCACTTTGTAAGAGAGCCCTTCAATGCGTATCAACCAACAGCAAC 2159
 QY 1235 TTTCCGTTCTTGAAGAGAGAGTTGCGCTATGGAACCTTCTTAACCTTGAGTCCGCTG 1294
 DB 2160 TTTCCGTTCTTGAAGAGAGAGTTGCGCTATGGAACCTTCTTCTTAACCTTGAGTCCGCTG 2219
 QY 1295 TTTCAGAAAGAGCGGAAACGTTGATTCCTTGAGAGAAATCCACCAAGAAACAACATG 1354
 DB 2220 TTTCAGAAAGAGCGGAAACGTTGATTCCTTGAGAGAAATCCACCAAGAAACAACATG 2279
 QY 1355 TGCACCCAGGAGAGATTTCTCCACAGGTTGAGCAGGTGTCATGTTCCGTTCCGAT 1414

DB 2280 TGCACCCAGGAGAGATTTCTCCACAGGTTGAGCCAGTGTCCATGTTCCGTTCCGAT 2339
 QY 1415 TGAGCAACAGTCCGATGAGATCATCAGAGCTCTATGTTCTCATGATTCATCTAGT 1474
 DB 2240 TGAGCAACAGTCCGATGAGATCATCAGAGCTCTATGTTCTCATGATTCATCTAGT 2339
 QY 1475 CTGAGTTCAACAAATATCTTCTCTCTCAAAATCACCAAAATCCAAATGACCAAGTCTA 1534
 DB 2400 CTGAGTTCAACAAATATCTTCTCTCTCAAAATCACCAAAATCCAAATGACCAAGTCTA 2459
 QY 1535 CTAACTTTGATCTGGAACCTTCTCTCTCAAAATCACCAAAATCCAAATGACCAAGTCTA 1594
 DB 2460 CTAACTTTGATCTGGAACCTTCTCTCTCAAAATCACCAAAATCCAAATGACCAAGTCTA 2519
 QY 1595 TTAGAAGACTTCTCTGCGAGATTTAGACACCTCAGAGTTAATCATCATCTGACACCTTT 1654
 DB 2520 TTAGAAGACTTCTCTGCGAGATTTAGACACCTCAGAGTTAATCATCATCTGACACCTTT 2579
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 DB 2580 CTAAAGATATGTTGTCAGAGATTTGTTAGCGATCTTACCACTTACTTGCAATTTCAACCT 2639
 QY 1715 CCATCGACGAGAGCTTATCAATCAGAGTTAATCTTCCGCAACCATGTCAGAGCGGACGA 1774
 DB 2640 CCATCGACGAGAGCTTATCAATCAGAGTTAATCTTCCGCAACCATGTCAGAGCGGACGA 2699
 QY 1775 ACTTGCAATCCGAGAGCTTCAAGAACCGTCTGTTCACTACTCTTCACTTCAAG 1834
 DB 2700 ACTTGCAATCCGAGAGCTTCAAGAACCGTCTGTTCACTACTCTTCACTTCAAG 2759
 QY 1835 GATCAAGGTTTCAACCTTACGCTCATGTTTCAATTTCTGCAATGAAGTGAATG 1894
 DB 2760 GATCAAGGTTTCAACCTTACGCTCATGTTTCAATTTCTGCAATGAAGTGAATG 2819
 QY 1895 ACCGATTTGATTTGCTCTCCGAGAGTACTTCAAGGCTGAGTACTGAGAAATTCATG 1954
 DB 2820 ACCGATTTGATTTGCTCTCCGAGAGTACTTCAAGGCTGAGTACTGAGAAATTCATG 2879
 QY 1955 T 1955
 DB 2880 T 2880

RESULT 6
 US-09-329-169-9
 ; Sequence 9, Application US/09329169
 ; Patent No. 6329575
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Simbaldi
 ; TITLE OF INVENTION: DNA Construct Containing Bacillus
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 6329575arlis Corporation
 ; STREET: 564 Morris Avenue
 ; CITY: Summit
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07901
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/329,169
 ; FILING DATE: 09-Jun-1999
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/042,426
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 7378 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: Complete sequence of pZ01502
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-329-169-9

Query Match 66.3%; Score 1848.2; DB 4; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 95 CCATGACACAAACCCAAACATCAACGAATGCATTCCATPAACCTGCTTGAGTAAACCAAG 154
DB 1020 CCATGACACAAACCCAAACATCAACGAATGCATTCCATPAACCTGCTTGAGTAAACCAAG 1079
QY 155 AAGTTGAAGTACTGGTGGAGAAACGATTTGAAACCGGTACACCTCCATCGACATCTCT 214
DB 1080 AAGTTGAAGTACTGGTGGAGAAACGATTTGAAACCGGTACACCTCCATCGACATCTCT 1139
QY 215 TGTCTTGACACAGTTTCTGCTCAGCAGATTGCTGCAGGTGCTGGTGGTCTGCTCGAC 274
DB 1140 TGTCTTGACACAGTTTCTGCTCAGCAGATTGCTGCAGGTGCTGGTGGTCTGCTCGAC 1199
QY 275 TAGTTGACATCATCTGGGGTATCTTTGGTCAATCTCAATGGGATGCTTCTGCTGCAAA 334
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QY 335 TTGACGATGATCAACGAGGATCGAAGGATGGCCAGGAAACGAGGCAATCTTAGT 394
DB 1260 TTGACGATGATCAACGAGGATCGAAGGATGGCCAGGAAACGAGGCAATCTTAGT 1319
QY 395 TGAAGATTGACAACTCTCAACAAATCTATGACAGAGCTTTCAGAGTGGGAAAGCG 454
DB 1320 TGAAGATTGACAACTCTCAACAAATCTATGACAGAGCTTTCAGAGTGGGAAAGCG 1379
QY 455 ATCTACTAACCAGCTCTCCGCGAGGAAATGCGTATTCATTCAACGACATGAACGCG 514
DB 1380 ATCTACTAACCAGCTCTCCGCGAGGAAATGCGTATTCATTCAACGACATGAACGCG 1439
QY 515 CCTTGACACAGCTATCCCATTTGTTGCGAGTCCAGAACATACCAAGTCTCTCTGTCG 574
DB 1440 CCTTGACACAGCTATCCCATTTGTTGCGAGTCCAGAACATACCAAGTCTCTCTGTCG 1499
QY 575 TGTACGTTCAAGCAGCTATCTTCACTCAGCGTCTTTCAGACCTTAAGCGTGGGCG 634
DB 1500 TGTACGTTCAAGCAGCTATCTTCACTCAGCGTCTTTCAGACCTTAAGCGTGGGCG 1559
QY 635 AAAAGTGGGATTCGATGCTGCAACCATCAATAGCCGTTTCAACGACCTTATAGCTGA 694
DB 1560 AAAAGTGGGATTCGATGCTGCAACCATCAATAGCCGTTTCAACGACCTTATAGCTGA 1619
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QY 755 GTCTGATTTAGAGATTGATTGATTAGTAAACCAACAGTTTCAGAGAGAAATTGACCTCAAG 814
DB 1680 GTCTGATTTAGAGATTGATTGATTAGTAAACCAACAGTTTCAGAGAGAAATTGACCTCAAG 1739
QY 815 TTTTGAACATTTGTCTCTCTTCCCGAATATGATCCCAAGACCTAACCTTACCGTACAG 874

DB 1740 TTTTGAACATTTGTCTCTCTTCCCGAATATGATCCCAAGACCTAACCTTACCGTACAG 1799
QY 875 TGTCCCAACTTACAGAGAAATCTATCTAACCCAGTTCTTGAGAACTTGACGGTAGCT 934
DB 1800 TGTCCCAACTTACAGAGAAATCTATCTAACCCAGTTCTTGAGAACTTGACGGTAGCT 1859
QY 935 TCCGTGTTCTGCCCAAGGATTCGAGGCTTCATCAGAGCCCACTTGATGACATCT 994
DB 1860 TCCGTGTTCTGCCCAAGGATTCGAGGCTTCATCAGAGCCCACTTGATGACATCT 1919
QY 995 TGAACAGCATTAATCTTACACCGAATCTCAACAGAGAGATTAATCTGCTGGACACC 1054
DB 1920 TGAACAGCATTAATCTTACACCGAATCTCAACAGAGAGATTAATCTGCTGGACACC 1979
QY 1055 AGATCATGGCTCTCCAGTTGATTCAGCGGCGCCAGTTTACCTTCTCTATGAAA 1114
DB 1980 AGATCATGGCTCTCCAGTTGATTCAGCGGCGCCAGTTTACCTTCTCTATGAAA 2039
QY 1115 CTATGGAAAACGCGCTCCACACACAGTATCGTTGCTCAATAGTGAAGGTCTTACA 1174
DB 2040 CTATGGAAAACGCGCTCCACACACAGTATCGTTGCTCAATAGTGAAGGTCTTACA 2099
QY 1175 GAACCTTGTCTTCCACCTTGATCAGAGACCTTCAATTCGGTATCAACACAGAAC 1234
DB 2100 GAACCTTGTCTTCCACCTTGATCAGAGACCTTCAATTCGGTATCAACACAGAAC 2159
QY 1235 TTTCCGTTCTTGAAGGAAACAGAGTTCCGCTATGAAACCTCTTCACTTGGCATCCGCTG 1294
DB 2160 TTTCCGTTCTTGAAGGAAACAGAGTTCCGCTATGAAACCTCTTCACTTGGCATCCGCTG 2219
QY 1295 TTTTACAGAAAGCGGAAACCGTTGATTCCTTGAAGAAATCCACACAGAACCAATG 1354
DB 2220 TTTTACAGAAAGCGGAAACCGTTGATTCCTTGAAGAAATCCACACAGAACCAATG 2279
QY 1355 TGCACACGAGGAAAGATTCCTCCACAGTTGAGCCAGTCCATGTTCCGTTCCGAT 1414
DB 2280 TGCACACGAGGAAAGATTCCTCCACAGTTGAGCCAGTCCATGTTCCGTTCCGAT 2339
QY 1415 TCACCAACAGTTCCGATGATCATCAGAGCTCTTAATGTTCTCATGATTCATGATG 1474
DB 2340 TCACCAACAGTTCCGATGATCATCAGAGCTCTTAATGTTCTCATGATTCATGATG 2399
QY 1475 CTGAGTTCAACAAATATCTTCTCTCTCAATTCACCAATCCCATTTGACCAAGTTA 1534
DB 2400 CTGAGTTCAACAAATATCTTCTCTCTCAATTCACCAATCCCATTTGACCAAGTTA 2459
QY 1535 CTAACCTTGGATCTGGAACCTCTGTCGTAAGAACGAGCTTCAACAGAGGTATATT 1594
DB 2460 CTAACCTTGGATCTGGAACCTCTGTCGTAAGAACGAGCTTCAACAGAGGTATATT 2519
QY 1595 TTAGAAGAACTTCTCTGCGCAGATTAAGCACTTCAGAGTTTAAATCATCTGACCACTT 1654
DB 2520 TTAGAAGAACTTCTCTGCGCAGATTAAGCACTTCAGAGTTTAAATCATCTGACCACTT 2579
QY 1655 CTCAAAGATATGCTGTCAGAGTTGTTTACCATCTTCAACCTTGAATTTCCACACT 1714
DB 2580 CTCAAAGATATGCTGTCAGAGTTGTTTACCATCTTCAACCTTGAATTTCCACACT 2639
QY 1715 CCATCGAAGGAAGGCTATCAATCAGGTTAACTTCCGCAACCATGTCAGGCGCAGCA 1774
DB 2640 CCATCGAAGGAAGGCTATCAATCAGGTTAACTTCCGCAACCATGTCAGGCGCAGCA 2699
QY 1775 ACTTGCAATCCGAGCTTTCAGAAACCGTCCGTTTCACTACTCTTCAACTTCTTAA 1834
DB 2700 ACTTGCAATCCGAGCTTTCAGAAACCGTCCGTTTCACTACTCTTCAACTTCTTAA 2759
QY 1835 GATCAAGGTTTTCACCTTACGCTCATGCTGTTCAATCTTGCGCAATGAATGATCAT 1894
DB 2760 GATCAAGGTTTTCACCTTACGCTCATGCTGTTCAATCTTGCGCAATGAATGATCAT 2819
QY 1895 ACCGATATGATTTGTGCTGCTGCGCAAGTTACTTCAAGGCTGAGTACTGAAATTCATGC 1954
DB 2820 ACCGATATGATTTGTGCTGCTGCGCAAGTTACTTCAAGGCTGAGTACTGAAATTCATGC 2879

QY 1955 T 1955
DB 2880 T 2880

RESULT 7

US-09-330-714A-9
Sequence 9, Application US/09330714A

Patent No. 6342660

GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Simibaldi

TITLE OF INVENTION: DNA Construct Containing Bacillus

Thuringiensis Gene

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESS: No. 6342660artis Corporation

STREET: 564 Morris Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/330,714A

FILING DATE: 11-Jun-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/042,426

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993

REFERENCE/DOCKET NUMBER: 135/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 541-8614

TELEFAX: (919) 541-8689

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 7378 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

IMMEDIATE SOURCE:

CLONE: Complete sequence of pZ01502

SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-09-330-714A-9

Query Match 66.3%; Score 1848.2; DB 4; Length 7378;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 95 CCATGACAAACCAACCAATCAACGAATGCAATTCATACAACTGTTGAGTAACCAAG 154
DB 1020 CCATGACAAACCAACCAATCAACGAATGCAATTCATACAACTGTTGAGTAACCAAG 1079
QY 155 AAGTTGAAGTACTGTTGAGAGAGCAATGAAACCGTTTACACTCCCATCGACATCTCT 214
DB 1080 AAGTTGAAGTACTGTTGAGAGAGCAATGAAACCGTTTACACTCCCATCGACATCTCT 1139
QY 215 TGTCTTGAACAGTTTCTGCTCAGGAGTTCTGTCAGAGTCTGAGTTCTGTTCTCGAC 274
DB 1140 TGTCTTGAACAGTTTCTGCTCAGGAGTTCTGTCAGAGTCTGAGTTCTGTTCTCGAC 1199
QY 275 TAGTTGACATCATCTGGGATATCTTTGTCATCTCAATGGAGATGATCCGATGCAAA 334

DB 1200 TAGTTGACATCATCTGGGATATCTTTGTCATCTCAATGGAGATGATTCCTGATGCAAA 1259
QY 335 TTGAGCAGTTGATCAACCAAGAGATCGAAGATTGCGCAGAGAACCAAGCCATCTTAGT 394
DB 1260 TTGAGCAGTTGATCAACCAAGAGATCGAAGATTGCGCAGAGAACCAAGCCATCTTAGT 1319
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DB 1320 TGAAGAGATTGAGCAATCTCTACCAATCTATGAGAGAGCTTGAAGAGTGGAGACCCG 1379
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DB 1560 AAAGTGGGAGTTGATGCTGCAACCAATCAATAGACCGTTTACCAAGCCTTACTAGCTGA 1619
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Qy 1835 GATCAAGGTTTTCACCTTACCGCTCATATGTTTCAATTTGCGCAATGAAGTATCATTTG 1894
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Db 2820 ACCGATGAGTTTGTGCTGCGGAGGTTACCTTCAGAGCTGAGTACTGAGATTCATGTC 2879
Qy 1955 T 1955
Db 2880 T 2880

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RESULT 8

US-09-328-826-9

Sequence 9, Application US/09328826

Patent No. 6399860

GENERAL INFORMATION:

APPLICANT: Ivin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi

TITLE OF INVENTION: DNA Construct Containing Bacillus

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESS: No. 639860artis Corporation

STREET: 564 Morris Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/328,826

FILING DATE: 09-Jun-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/042,426

FILING DATE: March 13, 1998

ATTORNEY/AGENT INFORMATION:

NAME: Hoxie, Thomas

REGISTRATION NUMBER: 32,993

REFERENCE/DOCKET NUMBER: 135/1

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: Complete sequence of p201502
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-328-826-9

Query Match 56.3%; Score 1848.2; DB 4; Length 7378;
Beet Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 95 CCATGCAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 154
Db 1020 CCATGCAACAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1079
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Db 1080 AAGTTGAAGTACTTGTGAGAGACGATTTGAACCGGTTACCTCCATGACATCTTCT 1139
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Qy 575 TGTAGGTTCAAGAGGATTAATCTTCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 634
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Db 1740 TTTTGACATTTGTTCTTCTTCCGAACTATGACTCCGAAACCTAACCTTATCCGTACAG 1799

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QY      875 TGTCCCACTTACAGAGAAATCTAATCAACCCAGTTCTTGAGAACTTCGACGGTAGCT 934
DB      1800 TGTCCCACTTACAGAGAAATCTAATCAACCCAGTTCTTGAGAACTTCGACGGTAGCT 1859
QY      935 TCCGTGCTTCCGCCAAGCTATCCAGAGGCTCATCAAGAGCCCACTGATGAGACATCT 994
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DB      1920 TGAACAGCATATACTATCAACCCAGTCTCAAGAGAGAGATTAATGATGATGAGACATCT 1979
QY      1055 AGATCATGGCTCTTCAGTGGATTCAGCGGAGCCGAGTTTACTCTTCTCTATGAGAA 1114
DB      1980 AGATCATGGCTCTTCAGTGGATTCAGCGGAGCCGAGTTTACTCTTCTCTATGAGAA 2039
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DB      2040 CTATGAGGAAAGCGCGCTCCACAACAACGTATCGTTGCTCACTAGGTAGGAGTGTCTACA 2099
QY      1175 GAACCTGTCTTCCCACTTGTATCAGAAAGACCTTCAATATGCGTATCAACAACAGCAAC 1234
DB      2100 GAACCTGTCTTCCCACTTGTATCAGAAAGACCTTCAATATGCGTATCAACAACAGCAAC 2159
QY      1235 TTTTCGTTCTTGACGGAACAGAGTTGCGCTATGAGAACTCTTCTTAACTTGGCCATCCGCTG 1294
DB      2160 TTTTCGTTCTTGACGGAACAGAGTTGCGCTATGAGAACTCTTCTTAACTTGGCCATCCGCTG 2219
QY      1295 TTTTACAGAAAGCGGAAACCGTGTATCTCTTGAGAGAAATCCCAACAGAAACAGATG 1354
DB      2220 TTTTACAGAAAGCGGAAACCGTGTATCTCTTGAGAGAAATCCCAACAGAAACAGATG 2279
QY      1355 TGCCACCCAGGAAAGATTTCTCCACAGGTTGAGGCAAGTGTCCATGTTCCGTTCCGAT 1414
DB      2280 TGCCACCCAGGAAAGATTTCTCCACAGGTTGAGGCAAGTGTCCATGTTCCGTTCCGAT 2339
QY      1415 TCAGCAACAGTTCCGTGACATCATCAAGCTCTATGTTCTCATGATTCATCGTAGTG 1474
DB      2340 TCAGCAACAGTTCCGTGACATCATCAAGCTCTATGTTCTCATGATTCATCGTAGTG 2399
QY      1475 CTGAGTTCAACAAATATCAATCTCTCTCTCAAAATACCAAAATCCCAATGAGCAAGTCA 1534
DB      2400 CTGAGTTCAACAAATATCAATCTCTCTCTCAAAATACCAAAATCCCAATGAGCAAGTCA 2459
QY      1535 CTAACTTGGATCTGGAACCTTCTGTCTGTAAGAAAGACAGGCTTTCACAGAGGTGATATTC 1594
DB      2460 CTAACTTGGATCTGGAACCTTCTGTCTGTAAGAAAGACAGGCTTTCACAGAGGTGATATTC 2519
QY      1595 TTAGAAGAACTTCTCTGCGCCAGATTTAGCAACCTCAAGATTAACTACTGACACACTTT 1654
DB      2520 TTAGAAGAACTTCTCTGCGCCAGATTTAGCAACCTCAAGATTAACTACTGACACACTTT 2579
QY      1655 CTGAAGAATATGCTGTCAGAGATTTGTTAGAGCATCAACCACTAACTGAACTTCCACACT 1714
DB      2580 CTGAAGAATATGCTGTCAGAGATTTGTTAGAGCATCAACCACTAACTGAACTTCCACACT 2639
QY      1715 CCATGACGGAAGGCTATCAATCAAGGTAACCTTCTCCGCAACATGTCAGCGGACAGA 1774
DB      2640 CCATGACGGAAGGCTATCAATCAAGGTAACCTTCTCCGCAACATGTCAGCGGACAGA 2699
QY      1775 ACTTGCAATCCGCGAGCTTCAGAAACCGTGGTTTCACTACTCTTTCAACTCTCTTAACG 1834
DB      2700 ACTTGCAATCCGCGAGCTTCAGAAACCGTGGTTTCACTACTCTTTCAACTCTCTTAACG 2759
QY      1835 GATCAAGGCTTTTACCCCTTAAGCGCTCATGTTCAATCTTGGAACAAGAGTGCATTTG 1894
DB      2760 GATCAAGGCTTTTACCCCTTAAGCGCTCATGTTCAATCTTGGAACAAGAGTGCATTTG 2819
QY      1895 ACCGTAATGAGTTTGTGCTGCGAAGTTACCTTCGAGGCTGAGTACTGAGAAATTCATGC 1954
DB      2820 ACCGTAATGAGTTTGTGCTGCGAAGTTACCTTCGAGGCTGAGTACTGAGAAATTCATGGA 2879
QY      1955 T 1955

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DB      2880 T 2880

RESULT 9
US-09-289-170-9
; Sequence 9, Application US/09289170
; Patent No. 6573438
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6573438artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/289.170
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/042,426
; FILING DATE: Match 13, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7378 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: Complete sequence of pZO1502
; US-09-289-170-9

Query Match      66.3%; Score 1848.2; DB 4; Length 7378;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1853; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY      95 CCATGACCAACACCCAAACATCAACGATTCATCACTGCTTGAATACCCAG 154
DB      1020 CCATGACCAACACCCAAACATCAACGATTCATCACTGCTTGAATACCCAG 1079
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Db 2220 TTTACAGAAAGAGCGGAACCGTTGATTCCTTGAAGAAATCCACACAGAACCAATG 2279
Qy 1355 TGCCACCCAGAGAGATTTCTCCACAGGTTGAGCCAGCTGTCATGTTCCGTTCCGAT 1414
Db 2280 TGCCACCCAGAGAGATTTCTCCACAGGTTGAGCCAGCTGTCATGTTCCGTTCCGAT 2339
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Db 2340 TCAGCAACAGTTCCGTTGAGCATCATCAGAGCTCTATGTTCTCATGAGATTCACTAGTG 2399

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Db 2640 CCATCGACGGAAGGCTCATATCAATCAGGTTAATCTTCCGAAACATGTCAGGCGGACA 2699
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Db 2700 ACTTGCAATCCGCGAGCTTCAGAACCGTCCGTTTCACTACTCTTCAACTTCTCTAACG 2759
Qy 1835 GATCAAGCGTTTTCACCTTAGCGCTCATGTTCAAATTTCTGCAATGAAGTTCATTTG 1894
Db 2760 GATCAAGCGTTTTCACCTTAGCGCTCATGTTCAAATTTCTGCAATGAAGTTCATTTG 2819
Qy 1895 ACCGTAATGATTTGTCCTGCGGAAGTTTACCTTCGAGGCTGAGTACTGAAATTCATGC 1954
Db 2820 ACCGTAATGATTTGTCCTGCGGAAGTTTACCTTCGAGGCTGAGTACTGAGATTCAGGA 2879
Qy 1955 T 1955
Db 2880 T 2880

RESULT 10
US-09-042-426-3
; Sequence 3, Application US/09042426
; Patent No. 6114608
; GENERAL INFORMATION:
; APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
; TITLE OF INVENTION: DNA Construct Containing Bacillus
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6114608artis Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,426
; FILING DATE: March 13, 1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoxie, Thomas
; REGISTRATION NUMBER: 32,993
; REFERENCE/DOCKET NUMBER: 135/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8614
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1851 base pairs
; TYPE: nucleic acid

STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 IMMEDIATE SOURCE:
 CLONE: cry1ab toxic gene region
 us-09-042-426-3

Query Match 66.2%; Score 1845.4; DB 3; Length 1851;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 96 CATGACACAAACCAACATCAAGATGATTCATCAACTGCTTGAATTAACCGA 155
 Db 1 CATGACACAAACCAACATCAAGATGATTCATCAACTGCTTGAATTAACCGA 60

QY 156 AGTTGAAGTCTTGGTGAAGAACGATTTGAACCGGTTACACTCCCATGACATCTCTT 215
 Db 61 AGTTGAAGTCTTGGTGAAGAACGATTTGAACCGGTTACACTCCCATGACATCTCTT 120

QY 216 GTCCCTGACACAGTTTCTGCTCAGCGAGTTGCTGCGAGGTTGGGTTGCTTCCGACT 275
 Db 121 GTCCCTGACACAGTTTCTGCTCAGCGAGTTGCTGCGAGGTTGGGTTGCTTCCGACT 180

QY 276 AGTTGACATCATCTGGGGTATCTTGGTTCATCTTCATGGATGGATCTCTGGTCAAT 335
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QY 336 TGAGCAGTTGATCAACAGAGAGTGAAGAGTTGCCAGGAACGAGCCATCTTAGATT 395
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QY 396 GGAAGGATTTGAGCATCTCTACCAATCTATGACAGAGCTTCAGAGTGGGAAAGCGA 455
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QY 456 TCCTACTAACCCAGCTCTCCGAGGAAGTGGTATTAATTCACAGCATGAACAGCGC 515
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QY 516 CTTGACCAAGCTATCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTTCTCGCT 575
 Db 421 CTTGACCAAGCTATCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTTCTCGCT 480

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 Db 781 GTCCCACTTACCAAGAAATCTATTAACCAAGTTCTTGAAGACTTGAAGGTAGCTT 840

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 Db 841 CCGTGGTTCTGCGCAAGGATGCAAGGCTCCATCAAGAGCCCAACTTATGACATCTT 900

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 Db 1141 TTCCGTTCTTGAAGGAAACAGAGTTGCTTGAAGGCTCTTCACTTGGCATCGCTGT 1200

QY 1296 TTACAGAAAGACGGAACCGTTGATTCCTTGAAGAAATCCACAGAAACAATGT 1355
 Db 1201 TTACAGAAAGACGGAACCGTTGATTCCTTGAAGAAATCCACAGAAACAATGT 1260

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 Db 1261 GCCACCCAGGCAAGGATTTCTCCACAGGTTGAGCCAGTGTCCATGTTCCGATTT 1320

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 Db 1441 TTAACCTTGATCTGGAACCTTCTGTGTGAAAGACAGGCTTCAAGAGGTATATCTT 1500

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 Db 1621 CATGACGGAAGGCTTATCAATCAAGGTAATTTCTCCGCAACATGTCAGCGGACGAA 1680

QY 1776 CTTGCAATCCGGGAGCTTCAAGACCGTCCGTTCACTACTGCTTCAACTCTCTAACGG 1835
 Db 1681 CTTGCAATCCGGGAGCTTCAAGACCGTCCGTTCACTACTGCTTCAACTCTCTAACGG 1740

QY 1836 ATCAAGGCTTTTCAACCTTACGCTCATGTTGTTCAATTTGCGCAATGAAGTGA 1895
 Db 1741 ATCAAGGCTTTTCAACCTTACGCTCATGTTGTTCAATTTGCGCAATGAAGTGA 1800

QY 1896 CCGTATGAGTTTGTGCTTCCGAAAGTATCACTTGAAGCTGAGTACT 1942
 Db 1801 CCGTATGAGTTTGTGCTTCCGAAAGTATCACTTGAAGCTGAGTACT 1847

RESULT 11
 US-09-291-238-3
 ; Sequence 3, Application US/09291238
 ; Patent No. 6222104
 ; GENERAL INFORMATION:
 ; APPLICANT: Irvin J. Metcalf, Paul S. Dietrich, Ralph Sinibaldi
 ; TITLE OF INVENTION: DNA Construct Containing Bacillus
 ; NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 622210artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/291,238
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: cry1ab toxic gene region
US-09-291-238-3

Query Match 66.2%; Score 1845.4; DB 3; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 96 CATGGACAACAACCCAAACATCAAGATTCATCAACATCTTGAGTAACCCAGA 155
DB 1 CATGGACAACAACCCAAACATCAAGATTCATCAACATCTTGAGTAACCCAGA 60
QY 156 AGTTGAAGTACTTGTTGGTGAAGAACGATTTGAAACCGGTTACACTCCCATCGACATCTCCTT 215
DB 61 AGTTGAAGTACTTGTTGGTGAAGAACGATTTGAAACCGGTTACACTCCCATCGACATCTCCTT 120
QY 216 GTCCCTGACACAGTTCTGCTCAGGAGGTTGCTGCAGGTCGTGGGTTCTGCTCGAGT 275
DB 121 GTCCCTGACACAGTTCTGCTCAGGAGGTTGCTGCAGGTCGTGGGTTCTGCTCGAGT 180
QY 276 AGTTGACATCACTGCGGGATCTTTGTCTCATCTCAATGGATGATTCCTGGTCAAT 335
DB 181 AGTTGACATCACTGCGGGATCTTTGTCTCATCTCAATGGATGATTCCTGGTCAAT 240
QY 336 TGAGCAGTTGATCAACCAAGATCGAAGAGTTCCGCAAGAACCGGCCATCTTAAGTT 395
DB 241 TGAGCAGTTGATCAACCAAGATCGAAGAGTTCCGCAAGAACCGGCCATCTTAAGTT 300
QY 396 GGAAGGATTTGAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGAGTGGAGCCGA 455
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DB 361 TCTTAATAACCCAGCTCTTCGCGAGGAAATGCGTATTCATTTCAAAGACATGAACAGCGC 420
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QY 576 GTAGCTTCAAGCAGCTATCTTCACTCAGCGTCTTGAGAGCTGTATGGGCA 635
DB 481 GTAGCTTCAAGCAGCTATCTTCACTCAGCGTCTTGAGAGCTGTATGGGCA 540
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QY 756 TCTGATTTAGAGATTGATTTAGATTAACAACCAAGTTCAGAGAGAAATGACCTCACAGT 815
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QY 816 TTTGAGACATTTGTTCTCTTCCGAACTATGATCCAGAACTTACCTTATCCGTACAGT 875
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DB 781 GTCCCACTTACAGAGAAATCTATTAACCCAGTTCTTGAAGAACTTCAGCGTAGCTT 840
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DB 1201 TTAAGAAAGAGCGGAACCGTTGATTCCTTGGAGGAATCCACACAGAAACAATGT 1260
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DB 1261 GCCACCCAGGCAAGGATTTCCCAACAGTTGAGCCAAGTTCATGTTCCGTTCCGAAAT 1320
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DB 1321 CAGCAACGTTCCGAGCATCATCAGAGCTCTATGTTCTCATGAGATTCAATCGTAGTGC 1380
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QY 1596 TAGAAGAACTTCTCTGAGCAGATTAGCAACCTCAAGATTAAATCATCTGACCACTTTC 1655
DB 1501 TAGAAGAACTTCTCTGAGCAGATTAGCAACCTCAAGATTAAATCATCTGACCACTTTC 1560

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QY 1716 CATGACGGAAGGCTTATCATCAGGTAATCTTCCGCAACATGTCAGCGGACGCA 1775
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QY 1836 ATCAAGCGTTTTCACCCCTTACCGCTCATGTCATTCATTCGCAATGAGTGAATTGA 1895
DB 1741 ATCAAGCGTTTTCACCCCTTACCGCTCATGTCATTCATTCGCAATGAGTGAATTGA 1800
QY 1896 CCGATTGAGTTTGTGCTGCTGCGCAAGTTACCTTGAGGCTGAGTACT 1942
DB 1801 CCGATTGAGTTTGTGCTGCTGCGCAAGTTACCTTGAGGCTGAGTACT 1847

RESULT 12

US-09-330-760-3
Sequence 3, Application US/09330760
Patent No. 6229075
GENERAL INFORMATION:
APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
TITLE OF INVENTION: DNA Construct Containing Bacillus
CORRESPONDENCE ADDRESS: 11
ADDRESSEE: No. 6229075artis Corporation
STREET: 564 Morris Avenue
CITY: Summit
STATE: New Jersey
COUNTRY: USA
ZIP: 07901
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/330,760
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: cry1ab toxic gene region
US-09-330-760-3

Query Match 66.2%; Score 1845.4; DB 3; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 96 CATGACACCAACACCACCAACATCAACGATGATTCCTTACACTGCTTGGTAACCGAGA 155
DB 1 CATGACACCAACACCACCAACATCAACGATGATTCCTTACACTGCTTGGTAACCGAGA 60
QY 156 AGTTGAAGTACTTGGTGGAGAAAGCAATTTGAACCGGTTTACATCCCATCGACATCTCCT 215
DB 61 AGTTGAAGTACTTGGTGGAGAAAGCAATTTGAACCGGTTTACATCCCATCGACATCTCCT 120
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Db      |||||
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1296 TTACAGAAAGAGCGGAACCGTTGATTCCTTGGAGGAAATCCACACAGAAACAATGT 1355
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1201 TTACAGAAAGAGCGGAACCGTTGATTCCTTGGAGGAAATCCACACAGAAACAATGT 1260
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1356 GCCACCCAGGGAAGGATTTCTCCCAAGGTTGAGCCAGCTGTCCATGTTCCGCTCGGATT 1415
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1476 TGAGTTCAACAATATCATTCCTCTCTCAATCAATCAACCCAAATCCCATTTGACCAAGTCTAC 1535
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1556 TCAAGATATCTGTGATGAGATTCTGTTACGATCTACCACTTAATCTGCAATTCACACCTC 1715
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1621 CATGACGGAGAGGCTATCAATCAAGGTAATCTTCTCCGCAACATGTCAGAGGAGCA 1680
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1681 CTTCGATTCGCGAGCTTCAGAACCGTGGTTTCACTACTCTCTTCAACTCTCTAACGG 1740
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1836 ATCAAGCGTTTTCACCTTAAGGCTCATGTGTTCAATCTGCGCAATGAAGTGTACATTTGA 1895
Db      |||||
1741 ATCAAGCGTTTTCACCTTAAGGCTCATGTGTTCAATCTGCGCAATGAAGTGTACATTTGA 1800
Qy      |||||
1896 CCGATTAGATTGTGCTGCGCGAAGTTACCTTGAAGGCTGAGTACT 1942
Db      |||||
1801 CCGATTAGATTGTGCTGCGCGAAGTTACCTTGAAGGCTGAGTACT 1847

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RESULT 13

US-09-328-473-3

Sequence 3, Application US/09328473

Patent No. 6232533

GENERAL INFORMATION:

APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi

TITLE OF INVENTION: DNA Construct Containing Bacillus

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6232533artis Corporation

STREET: 564 Morris Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/09/328,473
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,426
FILING DATE: March 13, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Hoxie, Thomas
REGISTRATION NUMBER: 32,993
REFERENCE/DOCKET NUMBER: 135/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1851 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: cry1ab toxic gene region
US-09-328-473-3
Query Match 66.2%; Score 1845.4; DB 3; Length 1851;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy      |||||
96 CATGACAAACCAACCAACATCAAGATGATTCATCAATCAATCTGAGTAACCCAGA 155
Db      |||||
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Qy      |||||
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Db      |||||
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 DB 1801 CCGTATGAGTTTGCGCTCCGAAAGTTTACCTTCGAGGCTGAGTACT 1847

 RESULT 14
 US-09-330-737-3
 : Sequence 3, Application US/09330737
 : Patent No. 6232534
 : GENERAL INFORMATION:
 : APPLICANT: Irvin J. Mettler, Paul S. Dietrich, Ralph Sinibaldi
 : TITLE OF INVENTION: DNA Construct Containing Bacillus
 : NUMBER OF SEQUENCES: 11
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: No. 6232534artis Corporation
 : STREET: 564 Morris Avenue
 : CITY: Summit
 : STATE: New Jersey
 : COUNTRY: USA
 : ZIP: 07901
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/09/330.737
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US/09/042.426
 : FILING DATE: March 13, 1998
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Hoxie, Thomas
 : REGISTRATION NUMBER: 32,993
 : REFERENCE/DOCKET NUMBER: 135/1
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (919) 541-8614
 : TELEFAX: (919) 541-8689
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 1851 base pairs
 : TYPE: nucleic acid
 : STRANDEDNESS: double
 : TOPOLOGY: linear
 : MOLECULE TYPE: DNA (genomic)
 : HYPOTHEICAL: NO
 : ANTI-SENSE: NO
 : IMMEDIATE SOURCE:
 : CLONE: cry1Ab toxic gene region
 : US-09-330-737-3

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 Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
:   LENGTH: 1851 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: double
:   TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: HYPOTHEetical: NO
: ANTI-SENSE: NO
: IMMEDIATE SOURCE:
: CLONE: cry1Ab toxic gene region
: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-329-169-3

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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1846; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-980-650-6

Perfect score: 2788
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Listing first 45 summaries

Database : Published Applications NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the total score distribution.
and is derived by analysis of the total score distribution.

SUMMARIES

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5	1411.8	50.6	3534	12	US-10-102-469-9
6	1411.8	50.6	3534	12	US-10-102-469-11
7	1411.8	50.6	3534	12	US-10-102-469-13
8	1328.8	47.7	1767	12	US-10-102-469-5
9	1220.4	43.8	4360	9	US-09-756-643-1
10	1220	43.8	3468	11	US-09-988-462-1
11	1197.6	43.0	3531	14	US-10-035-060-7
12	1194.4	42.8	3531	14	US-10-035-060-3
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14	1180.8	42.4	1743	12	US-10-102-469-1
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18	1152.2	41.3	3546	11	US-09-988-462-10	Sequence 10, Appl
19	1152.2	41.3	3546	11	US-09-988-462-12	Sequence 12, Appl
20	1152.2	41.3	3546	11	US-09-988-462-14	Sequence 14, Appl
21	1152.2	41.3	3546	11	US-09-988-462-16	Sequence 16, Appl
22	1152.2	41.3	3547	11	US-09-988-462-17	Sequence 17, Appl
23	1145.8	41.1	3468	11	US-09-988-462-2	Sequence 2, Appli
24	1088.6	39.0	4973	11	US-09-990-659A-15	Sequence 15, Appl
25	1029.6	36.9	3534	9	US-09-873-873-33	Sequence 33, Appl
26	1029.6	36.9	3534	12	US-10-365-645-33	Sequence 27, Appl
27	1026.4	36.8	3534	9	US-09-873-873-27	Sequence 27, Appl
28	1026.4	36.8	3534	11	US-09-997-914-27	Sequence 27, Appl
29	1026.4	36.8	3534	12	US-10-365-645-27	Sequence 25, Appl
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43	971.4	34.8	1839	9	US-09-826-660-17	Sequence 17, Appl
44	971.4	34.8	1839	9	US-09-826-660-18	Sequence 18, Appl
45	971.4	34.8	3468	9	US-09-826-660-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-10-102-469-7
Sequence 7, Application US/10102469
Publication No. US20030192078A1
GENERAL INFORMATION:
APPLICANT: Fischhoff, David A.
TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
FILE REFERENCE: 38-21 (13553) B
CURRENT APPLICATION NUMBER: US/10/102,469
PRIOR APPLICATION NUMBER: 2002-09-05
PRIOR FILING DATE: 1995-05-03
PRIOR APPLICATION NUMBER: 08/434,105
PRIOR FILING DATE: 1992-10-09
PRIOR APPLICATION NUMBER: 07/959,506
PRIOR FILING DATE: 1990-02-12
PRIOR APPLICATION NUMBER: 07/315,355
PRIOR FILING DATE: 1989-02-24
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 7
LENGTH: 1845
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: synthetic structural gene encoding an insecticidal protein of B
NAME/KEY: CDS
LOCATION: (1) ..(1845)
OTHER INFORMATION:
US-10-102-469-7
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1845, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
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Db 1 ATGACACAAACCCAAACATCAAGAAATGATTCATCAACTGCTTGAGTAACCCAGAA 60
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 Oy 457 CCTACTAACCAGCTCTCCGAGAGAAATGGGTATTCATTCACAGATGAACAGCC 516
 Db 361 CCTACTAACCAGCTCTCCGAGAGAAATGGGTATTCATTCACAGATGAACAGCC 420
 Oy 517 TTGACCAAGCATCCGATTTGTGCGATTCAGAACTCAAGTTCCTCTGTGCGGT 576
 Db 421 TTGACCAAGCATCCGATTTGTGCGATTCAGAACTCAAGTTCCTCTGTGCGGT 480
 Oy 577 TACGTTCAAGGAGCTAATCTTCACTCAGCGTCTTTCGAGAGCTTGTGGGCA 636
 Db 481 TACGTTCAAGGAGCTAATCTTCACTCAGCGTCTTTCGAGAGCTTGTGGGCA 540
 Oy 637 AGGTGGGATTCGATGCTGCAACCATCAATAGCCGTTCACAGACCTTACTAGCTGAT 696
 Db 541 AGGTGGGATTCGATGCTGCAACCATCAATAGCCGTTCACAGACCTTACTAGCTGAT 600
 Oy 697 GGAACATCAACGAGCAGCTGTTGTGTAACAACATGCTTGGAGCGTGTGGGAT 756
 Db 601 GGAACATCAACGAGCAGCTGTTGTGTAACAACATGCTTGGAGCGTGTGGGAT 660
 Oy 757 CCTGATTCAGATTTGATTAAGATTAACAACAGTTCAAGAGAAATTTGACCTCAAGT 816
 Db 661 CCTGATTCAGATTTGATTAAGATTAACAACAGTTCAAGAGAAATTTGACCTCAAGT 720
 Oy 817 TTGACATTTGTGTCTCTCTCCGAACTATGACTCAAGACCTTATCCGTACAGT 876
 Db 721 TTGACATTTGTGTCTCTCTCCGAACTATGACTCAAGACCTTATCCGTACAGT 780
 Oy 877 TCCCAACTTACAGAGAAATCTATTAACCAAGTTCCTTGAACCTTGAACGGTGTG 936
 Db 781 TCCCAACTTACAGAGAAATCTATTAACCAAGTTCCTTGAACCTTGAACGGTGTG 840
 Oy 937 CGTGTCTTCCCAAGATATGAGAGCTTCATCAGAGCCCACTTGAATGACATTTG 996
 Db 841 CGTGTCTTCCCAAGATATGAGAGCTTCATCAGAGCCCACTTGAATGACATTTG 900
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 Oy 1057 ATCATGAGCTCTCAAGTGTGATTCAGCGGAGCCGAGTTTACCTTCTCTATGAACT 1116
 Db 961 ATCATGAGCTCTCTCAAGTGTGATTCAGCGGAGCCGAGTTTACCTTCTCTATGAACT 1020
 Oy 1117 ATGGAAACGCGCTCCAAACACGATCTGTGCTCAACTAGGTCAAGGTTCTTACA 1176
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Db 1081 ACCTGTCTTCCACTTGTACAGAAAGACCTTCAATATCGGTATCAACACAGCACTT 1140
 Oy 1237 TCCGTTCTTGAACGGAACAGAGTTTGGCTTATGAAACCTTCTTAATCTTGCAATCCGCT 1296
 Db 1141 TCCGTTCTTGAACGGAACAGAGTTTGGCTTATGAAACCTTCTTAATCTTGCAATCCGCT 1200
 Oy 1297 TACGAAAGAGCGGAACCGTTGATTCCTTGGAGCAAAATCCCAACAGAACCAATGTG 1356
 Db 1201 TACGAAAGAGCGGAACCGTTGATTCCTTGGAGCAAAATCCCAACAGAACCAATGTG 1260
 Oy 1357 CCACCCAGGCAAGGATTTCTCCACAGGTGAGCCAGGTTCATGTTCCGTTCCGAGTTC 1416
 Db 1261 CCACCCAGGCAAGGATTTCTCCACAGGTGAGCCAGGTTCATGTTCCGTTCCGAGTTC 1320
 Oy 1417 AGCAACAGTTCCGAGCATCATAGAGCTCTATGTTCTCATAGATTCATCTGATGCT 1476
 Db 1321 AGCAACAGTTCCGAGCATCATAGAGCTCTATGTTCTCATAGATTCATCTGATGCT 1380
 Oy 1477 GAGTTCAACATATCATTTCTTCTCTCAATCAACCAATCCATTTGACCAAGTCTA 1536
 Db 1381 GAGTTCAACATATCATTTCTTCTCTCAATCAACCAATTTGACCAAGTCTA 1440
 Oy 1537 AACCTGATTCGGAATCTTGTGTGTAAGAGACAGGCTTCAGAGAGGTGATTTCTT 1596
 Db 1441 AACCTGATTCGGAATCTTGTGTGTAAGAGACAGGCTTCAGAGAGGTGATTTCTT 1500
 Oy 1597 AGAAGAACTTCTCCGAGCATTAAGCAACCTCAGAGTTAAATCATCTGACCACTTCT 1656
 Db 1501 AGAAGAACTTCTCCGAGCATTAAGCAACCTCAGAGTTAAATCATCTGACCACTTCT 1560
 Oy 1657 CAAGATATCTGTGAGGATTCGTTAGCATCTACCACTTAATTTGCAATTCACACTCT 1716
 Db 1561 CAAGATATCTGTGAGGATTCGTTAGCATCTACCACTTAATTTGCAATTTCAACTCTC 1620
 Oy 1717 ATGACGGAAGCCTTATCAATCAGGATTAATCTTCCCAACATGTAAGCGGAGCAAC 1776
 Db 1621 ATGACGGAAGCCTTATCAATCAGGATTAATCTTCCCAACATGTAAGCGGAGCAAC 1680
 Oy 1777 TTGCAATCCGAGCATTCAGAACCGTGGTTTCACTACTCTTCAACTTCTTCAACGA 1836
 Db 1681 TTGCAATCCGAGCATTCAGAACCGTGGTTTCACTACTCTTCAACTTCTTCAACGA 1740
 Oy 1837 TCAAGCGTTTACCTTGAAGCTATGTTCAATTTCTGCAATGAAGTATGATGAC 1896
 Db 1741 TCAAGCGTTTACCTTGAAGCTATGTTCAATTTCTGCAATGAAGTATGATGAC 1800
 Oy 1897 CGTATGAGTTTGTGCTGCGGAGGATTAATCTTGAAGCTGATGAC 1941
 Db 1801 CGTATGAGTTTGTGCTGCGGAGGATTAATCTTGAAGCTGATGAC 1845

RESULT 2
 US-09-988-462-5
 ; Sequence 5, Application US/09988462
 ; Publication No. US20030046726A1
 ; GENERAL INFORMATION:
 APPLICANT: Kozziel, Michael G.
 ; Debat, Nalini M.
 ; Lewis, Kelly S.
 ; Kramer, Vance C.
 ; Warren, Gregory W.
 ; Evola, Stephen V.
 ; Crossland, Lyle D.
 ; Wright, Martha S.
 ; Merlin, Ellis J.
 ; Iannis, Karen L.
 TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
 INSECTICIDAL ACTIVITY IN MAIZE
 NUMBER OF SEQUENCES: 94
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Syngenta Biotechnology, Inc.
 STREET: 3054 Cornwallis Road
 CITY: Research Triangle Park

```

STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/988,462
  FILING DATE: 20-NOV-2003
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: US 09/547,422
  FILING DATE: 11-APR-2000
  APPLICATION NUMBER: US 08/459,504
  FILING DATE: 02-JUN-1995
  APPLICATION NUMBER: US 07/951,715
  FILING DATE: 25-SEP-1992
  APPLICATION NUMBER: US 07/772,027
  FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
  NAME: Meigs, J. Timothy
  REGISTRATION NUMBER: 38,241
  REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (919) 541-8587
  TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 5:
  SEQUENCE CHARACTERISTICS:
    LENGTH: 1845 base pairs
    TYPE: nucleic acid
    STRANDEDNESS: single
    TOPOLOGY: linear
    MOLECULE TYPE: other nucleic acid
    DESCRIPTION: /desc = "Synthetic DNA"
    HYPOTHETICAL: NO
  FEATURE:
    NAME/KEY: misc feature
    LOCATION: 1..1845
    OTHER INFORMATION: /note= "This is the synthetic Bc
    gene according to Perlak et al. as shown in Figures 4 and 5 as
    PROMOT."
  SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-988-462-5
Query Match      66 1%; Score 1843.4; DB 11; Length 1845;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1844; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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457 CTTACTAACCCAGCTCTCCGAGAGAAATGCGTATTCATTTCAACGACATGAAACAGGCC 516
361 CCTACTAACCCAGCTCTCCGAGAGAAATGCGTATTCATTTCAACGACATGAAACAGGCC 420
517 TTGACCAAGCTATCCATGTTGCGAGTCCAGAACTACCAAGTTCCTCTGTCGGTG 576
421 TTGACCAAGCTATCCATGTTGCGAGTCCAGAACTACCAAGTTCCTCTGTCGGTG 480
577 TACGTTCAAGCAGCTAATCTTCACTCAGGCGTCTGAGACGTTAGCGTGTGGGCAA 636
481 TACGTTCAAGCAGCTAATCTTCACTCAGGCGTCTGAGACGTTAGCGTGTGGGCAA 540
637 AGTGGGAGTTGATGCTGCAACCATATBACCCTTACAACGACCTTACTAGGCTATT 696
541 AGTGGGAGTTGATGCTGCAACCATATBACCCTTACAACGACCTTACTAGGCTATT 600
697 GGAACCTACACCCGACACGCGTGTGTTGGTACAACTGGCTTGGAGCGGTGGGGGT 756
601 GGAACCTACACCCGACACGCGTGTGTTGGTACAACTGGCTTGGAGCGGTGGGGGT 660
757 CCTGATTCAGAGATTGGAATTAGATACACAGTTTCAGAGAGATTGACCCCTCAGATT 816
661 CCTGATTCAGAGATTGGAATTAGATACACAGTTTCAGAGAGATTGACCCCTCAGATT 720
817 TTGACATATGTGTCTCTTCCGAACTATGACTTCAGAACTTACCCCTATCCGTACAGTG 876
721 TTGACATATGTGTCTCTTCCGAACTATGACTTCAGAACTTACCCCTATCCGTACAGTG 780
877 TCCCACTTACAGAGAAATCTATACATACCAATCTTGAACCTTCAAGGATGCTC 936
781 TCCCACTTACAGAGAAATCTATACATACCAATCTTGAACCTTCAAGGATGCTC 840
937 CGTGTCTCGCCAGGATGCAAGGCTCCATCAGAGCCCACTTGATGAGATCTTG 996
841 CGTGTCTCGCCAGGATGCAAGGCTCCATCAGAGCCCACTTGATGAGATCTTG 900
997 AACAGCATATCTATCTACACGATGCTTCAACAGAGAGATTAATGCTCTGACACCAAG 1056
901 AACAGCATATCTATCTACACGATGCTTCAACAGAGAGATTAATGCTCTGACACCAAG 960
1057 ATCATGGCCTCTCCAGTTGATGATGAGGCGGCGAGTTTACTTCTCTTATGGAAT 1116
961 ATCATGGCCTCTCCAGTTGATGATGAGGCGGCGAGTTTACTTCTCTTATGGAAT 1020
1117 ATGGAAACGCGCTCCCAACAAAGTATCGTCTCACTAGGTACAGGGTGTCTACAGA 1176
1021 ATGGAAACGCGCTCCCAACAAAGTATCGTCTCACTAGGTACAGGGTGTCTACAGA 1080
1177 ACCTTGTCTTCCACTGTGTACAGAAAGCCCTTCAATATCGGTATCAACACAGCACTT 1236
1081 ACCTTGTCTTCCACTGTGTGTACAGAAAGCCCTTCAATATCGGTATCAACACAGCACTT 1140
1237 TCCGTTCTTGAACGAAAGATTTGGCTATGGAACCTTCTTACTTGGCATCCGCTGT 1296
1141 TCCGTTCTTGAACGAAAGATTTGGCTATGGAACCTTCTTACTTGGCATCCGCTGT 1200
1297 TACGAAAGACGGAACCGTGTATCTTGGACGAAATCCCAACACAGAAACATATG 1356
1201 TACGAAAGACGGAACCGTGTATCTTGGACGAAATCCCAACACAGAAACATATG 1260
1357 CCACCAGGACGAAATTTCCCAACAGTTGAGCCAGTGTCTCATGTTCCGTTCCGATTC 1416
1261 CCACCAGGACGAAATTTCCCAACAGTTGAGCCAGTGTCTCATGTTCCGTTCCGATTC 1320
1417 AGCAACAGTTCCGAGAGATCATGAGAGCTCTATGTTCTATGATTCATCGTAGTCT 1476
1321 AGCAACAGTTCCGAGAGATCATGAGAGCTCTATGTTCTATGATTCATCGTAGTCT 1380
1477 GAGTTCAACAATATCATCTTCTCTCAAAATCAACCAATTCATGACCAAGTCTA 1536
1381 GAGTTCAACAATATCATCTTCTCTCAAAATCAACCAATTCATGACCAAGTCTA 1440

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Oy	1537	AACCTGGATCTCGAACTTCGTGGTGAAGAACACAGGCTTCACAGGAGGTGATATCTT	1596
Db	1441	AACCTGGATCTGGAACCTTCGTGGTGAAGAACACAGGCTTCACAGGAGGTGATATCTT	1500
Oy	1597	AGAAGAACTTCTCGGCGCAGATTAGCACCCCTCAGAGTTAAATCATCATCGACCACTTCT	1656
Db	1501	AGAAGAACTTCTCGGCGCAGATTAGCACCCCTCAGAGTTAAATCATCATCGACCACTTCT	1560
Oy	1657	CAAGGATATCGTGTACGAGATTGGTTACGCATCTACCACTAACTTGCAATTCACAACCTCC	1716
Db	1561	CAAGGATATCGTGTACGAGATTGGTTACGCATCTACCACTAACTTGCAATTCACAACCTCC	1620
Oy	1717	ATCGACGGAAGGCTTATCATCAGGGTAATTTTCCGCAACCATGTCAAGGGGACGAAAC	1776
Db	1621	ATCGACGGAAGGCTTATCATCAGGGTAATTTTCCGCAACCATGTCAAGGGGACGAAAC	1680
Oy	1777	TTGCAATCCGGCAGCTTCAGAACCGTCGGTTTCACTACTCTCTTCAACTTCTCTAAACGA	1836
Db	1681	TTGCAATCCGGCAGCTTCAGAACCGTCGGTTTCACTACTCTCTTCAACTTCTCTAAACGA	1740
Oy	1837	TCAAGCGTTTTCACCCCTTAGCGGCTCATGTGTTCAATTCGSCAAATGAAGTGTACATTGAC	1896
Db	1741	TCAAGCGTTTTCACCCCTTAGCGGCTCATGTGTTCAATTCGSCAAATGAAGTGTACATTGAC	1800
Oy	1897	CGTATGAGTTTGTCCTCCCGGAAGTTACCTTCAGGCTGAGTAC	1941
Db	1801	CGTATGAGTTTGTCCTCCCGGAAGTTACCTTCAGGCTGAGTAC	1845

RESULT 3

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US-10-102-469-23
; Sequence 23, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fieschoff, David A.
; APPLICANT: Petiak, Frederick J.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT APPLICATION NUMBER: US/10/102,469
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 3531
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic structural gene encoding a fusion protein derived from
; FEATURE:
; OTHER INFORMATION: B.t.k. HD-1 and B.t.k. HD-73
; NAME/KEY: CDS
; LOCATION: (1)..(3531)
; OTHER INFORMATION:
US-10-102-469-23

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Query Match	66.1%	Score 1843.4	DB 12	Length 3531
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1844; Conservative	0	Mismatches 1	Indels 0	Gaps 0

QY 97 ATGACAAACCCCAAATCATCAAGATGATTCATACAACTGTTAGTAAACCAAGA 156

Db 1 ATGACAAACCAACCCCAAATCATCAAGATGATTCATACAACTGTTAGTAAACCAAGA 60

QY 157 GTTGAAGTACTTGGTGGAGAACGCATTTGAACCCGGTTACATCTCCATGCAATCTTCCTTG 216

Db	61	GTGGAAGTACTGTTGGTGGAGAACGATGTAAACCGGTTACACTCCATCGACATCTCCTTG	120
Qy	217	TCCTTGCACACGTTTCTTGCTCAAGCAAGTTGTGTCCAGGTGCTGGGTTCTGTTCTCGACTA	276
Db	121	TCCTTGGACACAGTTTCTGCTCAAGCAAGTTGTGTCCAGGTGCTGGGTTCTGTTCTCGACTA	180
Qy	277	GTTGACATCATCTGGGGGTACTCTTGGTGCATCTCAATGGAGTGCATCTCGTGAGCAATT	336
Db	181	GTTGACATCATCTGGGGGTACTCTTGGTGCATCTCAATGGAGTGCATCTCGTGAGCAATT	240
Qy	337	GAGCAGTTGATCAACCAAGAGATCGAAGAGTTGCGCAGGAACAGGCCATCTTAGTTG	396
Db	241	GAGCAGTTGATCAACCAAGAGATCGAAGAGTTGCGCCAGGAACAGGCCATCTTAGTTG	300
Qy	397	GAAGAGTTGGACATCTCTACCAAACTATGACAGAGGCTTCAGAGGTGGGAAGCCGAT	456
Db	301	GAAGAGTTGGACATCTCTACCAAACTATGACAGAGGCTTCAGAGGTGGGAAGCCGAT	360
Qy	457	CCTACTAACCCAGCTCTCCGCGAGAGAAATCGTATTCAATTCAACGACATGAACAGCGCC	516
Db	361	CCTACTAACCCAGCTCTCCGCGAGAGAAATCGTATTCAATTCAACGACATGAACAGCGCC	420
Qy	517	TTGACCAACAGCTATCCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTCTGTCCGTG	576
Db	421	TTGACCAACAGCTATCCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTCTGTCCGTG	480
Qy	577	TACGTTCAAGAGCTATCTTCAACCTGAGCGTGCTTGAAGCGTTACGTTTAGGCA	636
Db	481	TACGTTCAAGAGCTATCTTCAACCTGAGCGTGCTTGAAGCGTTTAGGCA	540
Qy	637	AGTGGGGATTCGATGCTGCAACCATCATAGCCGTTTACAACAAGCATTTACTAGCTGATT	696
Db	541	AGTGGGGATTCGATGCTGCAACCATCATAGCCGTTTACAACAAGCATTTACTAGCTGATT	600
Qy	697	GGAACATCAACCCGACCAAGCGTTTCGTTGGTAAACAATGAGCTTGAGCGGTGTGGGGT	756
Db	601	GGAACATCAACCCGACCAAGCGTTTCGTTGGTAAACAATGAGCTTGAGCGGTGTGGGGT	660
Qy	757	CCTGATTCCTAGAGATTGGATTAGTATACAAACAGTTCCAGAGAGATTGACCTTCACAGTT	816
Db	661	CCTGATTCCTAGAGATTGGATTAGTATACAAACAGTTCCAGAGAGATTGACCTTCACAGTT	720
Qy	817	TTGACACATTGTGTCTCTCTTCCCGAATATAGACTCCAGAACTTACCTTATCCGACAGTG	876
Db	721	TTGACACATTGTGTCTCTCTTCCCGAATATAGACTCCAGAACTTACCTTATCCGACAGTG	780
Qy	877	TCCCAACTTACAGAGAAATCTATACTAAACCAAGTTCTTAGAGAACTTCGACGGTAGCTTC	936
Db	781	TCCCAACTTACAGAGAAATCTATACTAAACCAAGTTCTTAGAGAACTTCGACGGTAGCTTC	840
Qy	937	CGTGGTTCGCGCAAGGATTCGAAGGCTCATCGAGGCCCAACTTGTATGACATCTTG	996
Db	841	CGTGGTTCGCGCAAGGATTCGAAGGCTCATCGAGGCCCAACTTGTATGACATCTTG	900
Qy	997	AACAGCATTAATCTATCAACCGAGCTCAACAGAGAGATTTATCTGCTCGACACACAG	1056
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Db	961	ATCATGGGCTTCCAGTTGGAATTGACGGGGCCGAGTTTACCTTCTCTTATGAACT	1020
Qy	1117	ATGGGAAACCGCGTCCACACAAACGATATGCTTCTCAATAGGTCAAGGAGTGTACAGA	1176
Db	1021	ATGGGAAACCGCGTCCACACAAACGATATGCTTCTCAATAGGTCAAGGAGTGTGTACAGA	1080
Qy	1177	ACCTTGTCTTCCACCTTGTACAGAAAGCCCTTCAATATCGGTATCAACACACAGCAACT	1236
Db	1081	ACCTTGTCTTCCACCTTGTACAGAAAGCCCTTCAATATCGGTATCAACACACAGCAACT	1140
Qy	1237	TCCGTTCTTACGGAACAGAGTTTGCGCTATAGGAACCTTCTTAACCTTGCAATCGCGTGT	1296
Db	1141	TCCGTTCTTACGGAACAGAGTTTGCGCTATAGGAACCTTCTTAACCTTGCAATCGCGTGT	1200

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QY 1297 TACAGAAAGAGCGGAAACCGTTGATTCTCTGGACGAAATCCCAACAGAAACAAATGTG 1356
DB 1201 TAGAGAAAGAGCGGAAACCGTTGATTCTCTGGACGAAATCCCAACAGAAACAAATGTG 1260
QY 1357 CCACCCAGGCAAGATTTCTCCCAAGGTTGAGCCAGCTGTCCATGTTCCGTTCCGATTC 1416
DB 1261 CCACCCAGGCAAGATTTCTCCCAAGGTTGAGCCAGCTGTCCATGTTCCGTTCCGATTC 1320
QY 1417 AGCAACGTTCCGAGAGCATCATAGAGCTCTATGTTCTCATGATTCATGATGCT 1476
DB 1321 AGCAACGTTCCGAGAGCATCATAGAGCTCTATGTTCTCATGATTCATGATGCT 1380
QY 1477 GAGTTCAACATATCATCTCTCTCTCAATCAACCAATCCATTCGATGACCAAGCTACT 1536
DB 1381 GAGTTCAACATATCATCTCTCTCTCAATCAACCAATCCATTCGATGACCAAGCTACT 1440
QY 1537 AACCTGGATCTGGAATCTTCTGTGTGAAGAGACAGGCTTCAAGAGGTGATTTCTT 1596
DB 1441 AACCTGGATCTGGAATCTTCTGTGTGAAGAGACAGGCTTCAAGAGGTGATTTCTT 1500
QY 1597 AGAAGAACTTCTCCGAGCAGATTAGACACCTCAAGATTACATCACTGACCACTTCT 1656
DB 1501 AGAAGAACTTCTCCGAGCAGATTAGACACCTCAAGATTACATCACTGACCACTTCT 1560
QY 1657 CAAGATATCGTTCAGGATTCGTTACGCAATCACTCACTCACTTCACTCACTCTCC 1716
DB 1561 CAAGATATCGTTCAGGATTCGTTACGCAATCACTCACTCACTTCACTCACTCTCC 1620
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DB 1621 ATCGACGAGAGGCTATATCAATCAAGGTAATCTTCCGCAACCATGTCAAGGCGAGCAAC 1680
QY 1777 TTGCAATCCGAGAGTTCAGAACGCTGGTTTCACTACTCTCTCACTTCACTTCACTCAAGGA 1836
DB 1681 TTGCAATCCGAGAGTTCAGAACGCTGGTTTCACTACTCTCTCACTTCACTTCACTCAAGGA 1740
QY 1837 TCAAGCGTTTTCACCCCTTAGGCTCATGTTCATTTGCGCAATGAGTGAATGTATGAC 1896
DB 1741 TCAAGCGTTTTCACCCCTTAGGCTCATGTTCATTTGCGCAATGAGTGAATGTATGAC 1800
QY 1897 CGTATGAGTTTGTGCTGCTGCGAAGTTAATCTTGAAGCTGAGTAC 1941
DB 1801 CGTATGAGTTTGTGCTGCTGCGAAGTTAATCTTGAAGCTGAGTAC 1845

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RESULT 4

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US-10-102-469-3
; Sequence 3, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; APPLICANT: Perlak, Frederick J.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT APPLICATION NUMBER: US/10/102,469
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic structural gene encoding B.t.k. HD-1 insecticidal prote

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; OTHER INFORMATION: in
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1920)
; OTHER INFORMATION:
US-10-102-469-3

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Query Match 50.6%; Score 1411.8; DB 12; Length 1920;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1453; Conservative 0; Mismatches 47; Indels 3; Gaps 1;

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QY 97 ATGACAAACAACCAACATCAAGATGCAATTCATCAACATCTGAGTAACCCGAA 156
DB 1 ATGACAAACAACCAACATCAAGATGCAATTCATCAACATCTGAGTAACCCGAA 60
QY 157 GTTGAAGTACTGTGTGAGAGAACGATGAAACGGGTATACACTCCATCGACATCTCTTG 216
DB 61 GTTGAAGTACTGTGTGAGAGAACGATGAAACGGGTATACACTCCATCGACATCTCTTG 120
QY 217 TCCTTGAACAAGTTTCTGCTCAAGAGTTCGTGCTGAGTGTGTTCTTCTGAGTA 276
DB 121 TCCTTGAACAAGTTTCTGCTCAAGAGTTCGTGCTGAGTGTGTTCTTCTGAGTA 180
QY 277 GTTGAACATCTGTGGGTATCTTGTGTCATCTCAATGAGATGCAATCTCTGTCGAAAT 336
DB 181 GTTGAACATCTGTGGGTATCTTGTGTCATCTCAATGAGATGCAATCTCTGTCGAAAT 240
QY 337 GAGCAGTTGATCAACAGAGATGCAAGAGTTGCGCCAGAGAACAGGCACTCTAGGTTG 396
DB 241 GAGCAGTTGATCAACAGAGATGCAAGAGTTGCGCCAGAGAACAGGCACTCTAGGTTG 300
QY 397 GAAGATTTAGCAATCTCTTACCAATCTATGAGAGAGCTTCAAGAGTGGAAAGCGAT 456
DB 241 GAAGATTTAGCAATCTCTTACCAATCTATGAGAGAGCTTCAAGAGTGGAAAGCGAT 300
QY 301 GAAGATTTAGCAATCTCTTACCAATCTATGAGAGAGCTTCAAGAGTGGAAAGCGAT 360
DB 457 CCTTCTAACCCAGCTCTCCGAGAGAAATGCTTCAATTCATCAACGACATGAACGCC 516
QY 361 CCTTCTAACCCAGCTCTCCGAGAGAAATGCTTCAATTCATCAACGACATGAACGCC 420
DB 517 TTGACCAAGCTATCCCATTTGTCGAGTCCAGAACTCAAGTTCCTCTTGTGCGTG 576
QY 421 TTGACCAAGCTATCCCATTTGTCGAGTCCAGAACTCAAGTTCCTCTTGTGCGTG 480
DB 577 TACGTTCAAGCAGTAATCTTCACTCAAGCTGCTTCAAGAGCTTGTGCGTGA 636
QY 481 TACGTTCAAGCAGTAATCTTCACTCAAGCTGCTTCAAGAGCTTGTGCGTGA 540
QY 637 AGTGGGATTCGATGCTGCAACCATCAATAGCCGTTTCAACGACCTTACTAGCTGAT 696
DB 541 AGTGGGATTCGATGCTGCAACCATCAATAGCCGTTTCAACGACCTTACTAGCTGAT 600
QY 697 GGAACATCAACGACGCTGTTGTTGTATCAACACTGCTTGAAGCGTGTGCGGAT 756
DB 601 GGAACATCAACGACGCTGTTGTTGTATCAACACTGCTTGAAGCGTGTGTGCGGAT 660
QY 757 CCTGATTTAGAGATTGATGATATCAACAGTTCAAGAGAAATTAACCTTCAAGTT 816
DB 661 CCTGATTTAGAGATTGATGATATCAACAGTTCAAGAGAAATTAACCTTCAAGTT 720
QY 817 TTGACATTTGTGCTCTCTCCGAACTATGATCTCAAGACTTACCTTACTGTCAGAG 876
DB 721 TTGACATTTGTGCTCTCTCCGAACTATGATCTCAAGACTTACCTTACTGTCAGAG 780
QY 877 TCCCAACTTACAGAGAAATCTATATCAACCGAGTTCTTGAACCTTGAAGCGTGA 936
DB 781 TCCCAACTTACAGAGAAATCTATATCAACCGAGTTCTTGAACCTTGAAGCGTGA 840
QY 937 CGTGGTTCTGCCAAAGTATGAGAGCTTCATCAGAGCCCACTTGAATGACATCTTG 996
DB 841 CGTGGTTCTGCCAAAGTATGAGAGCTTCATCAGAGCCCACTTGAATGACATCTTG 900
QY 997 AACGCAATATATATCAACGAGTCTCAGAGAGAGATTAATGATGTCGACACGAG 1056

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Db 901 AACAGCATATCTATCTACCCGATGCTCACAGAGAGATATTACTGTCTGACACACCAG 960
QY 1057 ATCATGCGCTCTCCAGTTGATGATGAGCGGAGCCGAGTTTAACTTCTCTCTATGAACT 1116
Db 961 ATCATGCGCTCTCCAGTTGATGATGAGCGGAGCCGAGTTTAACTTCTCTCTATGAACT 1020
QY 1117 ATGGAAACGCCGCTCCACAAACAGTATCGTTGCTCAAGTAGGTCAAGGTGTCTACAGA 1176
Db 1021 ATGGAAACGCCGCTCCACAAACAGTATCGTTGCTCAAGTAGGTCAAGGTGTCTACAGA 1080
QY 1177 ACCTTGCTTCCACCTTGTACAGAAAGCCCTTAATATCGGTATCAACAGCAAGAACTT 1236
Db 1081 ACCTTGCTTCCACCTTGTACAGAAAGCCCTTAATATCGGTATCAACAGCAAGAACTT 1140
QY 1237 TCCGTTCTTGACGAAACAGAGTTGCGCTATGAAACCTTCTTAACTTCCATCCGCTGT 1296
Db 1141 TCCGTTCTTGACGAAACAGAGTTGCGCTATGAAACCTTCTTAACTTCCATCCGCTGT 1200
QY 1297 TACAGAAAGACCGGAACCGTTGATTCTTGGACGAATCCACACAGAAACAATATGTG 1356
Db 1201 TACAGAAAGACCGGAACCGTTGATTCTTGGACGAATCCACACAGAAACAATATGTG 1260
QY 1357 CCACCCAGGCAAGATTCTCCACAGGTTGAGCCACGTGTCATGTTCCTTCGGATTTC 1416
Db 1261 CCACCCAGGCAAGATTCTCCACAGGTTGAGCCACGTGTCATGTTCCTTCGGATTTC 1320
QY 1417 AGCAACAGTTCCGAGAGCATATCAGAGCTCTATGTTCTCATGAGTATCATGTAGTCT 1476
Db 1321 AGCAACAGTTCCGAGAGCATATCAGAGCTCTATGTTCTCTTGATACACCGTAGTCT 1380
QY 1477 GAGTTCAACAATATCATCTCTCTCTCTCAATCACCACCAATCCCATGACCAAGTCTACT 1536
Db 1381 GAGTTCAACAATATCATCTCTCTCTCTCAATCACCACCAATCCCATGAGTAAAG---GGA 1437
QY 1537 AACCTTGATCTGGAATCTTCTGTGCTGAAAGACCAAGCTTCAACAGAGATATTTCTT 1596
Db 1438 AACCTTCTCTCAACGTTCTGTCAATTCAGAGCAGAGATTCATCTGTGAGAACCTCGTT 1497
QY 1597 AGA 1599
Db 1498 AGA 1500

RESULT 5
US-10-102-469-9
; Sequence 9, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; APPLICANT: Perlak, Frederick J.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT APPLICATION NUMBER: US/10/102,469
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic structural gene encoding an insecticidal protein derive
; NAME/KEY: CDS

; LOCATION: (1) .. (3534)
; OTHER INFORMATION:
US-10-102-469-9
Query Match 50.6%; Score 1411.8; DB 12; Length 3534;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1453; Conservative 0; Mismatches 47; Indels 3; Gaps 1;
QY 97 ATGACAAACAACCCAAACATCAAGAAATGCAATTCATACAACTGCTTGAATACCCAGAA 156
Db 1 ATGACAAACAACCCAAACATCAAGAAATGCAATTCATACAACTGCTTGAATACCCAGAA 60
QY 157 GTTGAAGTACTTGTGTGGAAGACGATTGAAACCGGTTACATCTCCCATGCAATCTCTTG 216
Db 61 GTTGAAGTACTTGTGTGGAAGACGATTGAAACCGGTTACATCTCCCATGCAATCTCTTG 120
QY 217 TCCTTGACAGATTTCCTGACGAGAGTTCGTGACAGGTGCTGGGTTGCTTCGAGACTA 276
Db 121 TCCTTGACAGATTTCCTGACGAGAGTTCGTGACAGGTGCTGGGTTGCTTCGAGACTA 180
QY 277 GTTGACATCATCTGGGGATATCTTTGTCATCTCAATGGAGATGCAATTCCTGGTCAAAAT 336
Db 181 GTTGACATCATCTGGGGATATCTTTGTCATCTCAATGGAGATGCAATTCCTGGTCAAAAT 240
QY 337 GAGCAGTTGATCAACACAGAGATGAGAGTTCCGACAGAAACAGGCCATCTTAGTTG 396
Db 241 GAGCAGTTGATCAACACAGAGATGAGAGTTCCGACAGAAACAGGCCATCTTAGTTG 300
QY 397 GAAGATGACCAATCTCTACCAATCTATGACAGACTTCAGAGATGGGGAAGCCGAT 456
Db 301 GAAGATGACCAATCTCTACCAATCTATGACAGACTTCAGAGATGGGGAAGCCGAT 360
QY 457 CCTACTAACCCAGCTCTCCGAGAGAAATGCGTATTCATTCACATCAACGATCAACAGCGCC 516
Db 361 CCTACTAACCCAGCTCTCCGAGAGAAATGCGTATTCATTCACATCAACGATCAACAGCGCC 420
QY 517 TTGACCAAGCTATTCCTATGTTGCGAGTCCAGAACTACCAAGTTCTCTCTTGTCCGTG 576
Db 421 TTGACCAAGCTATTCCTATGTTGCGAGTCCAGAACTACCAAGTTCTCTCTTGTCCGTG 480
QY 577 TACGTTCAAGAGCATTAATCTTCACTCAGCGGCTTCGAGAGTTAGCGTGTGTTGGGCA 636
Db 481 TACGTTCAAGAGCATTAATCTTCACTCAGCGGCTTCGAGAGTTAGCGTGTGTTGGGCA 540
QY 637 AGGTGGGATTCGATGCTGCAACCATCAATAGCCGTTACACGACCTTACTAGGCTGAT 696
Db 541 AGGTGGGATTCGATGCTGCAACCATCAATAGCCGTTACACGACCTTACTAGGCTGAT 600
QY 697 GGAACCTACACCCAGCAGCTGTTGTTGTTGTAACAACACTGCTTGGAGCGTGTGCGGT 756
Db 601 GGAACCTACACCCAGCAGCTGTTGTTGTTGTAACAACACTGCTTGGAGCGTGTGCGGT 660
QY 757 CCTGATTTAGAGATTGATTAATACCAACGATTCAAGAGAAATGACCTCCACAGTT 816
Db 661 CCTGATTTAGAGATTGATTAATACCAACGATTCAAGAGAAATGACCTCCACAGTT 720
QY 817 TTGACATTTGTCTCTCTTCCGAATATGACTCCAGAACCTTACCTATCCGTAAGTG 876
Db 721 TTGACATTTGTCTCTCTTCCGAATATGACTCCAGAACCTTACCTATCCGTAAGTG 780
QY 877 TCCCAACTTACAGAGAAATCTATTAACCAAGTTCTTGAACATTTGACAGGTAGCTTC 936
Db 781 TCCCAACTTACAGAGAAATCTATTAACCAAGTTCTTGAACATTTGACAGGTAGCTTC 840
QY 937 CGTGTTCGCCCAAGGATGAGAGGCTTCATCAGAGCCACACTTGTATGACATCTTG 996
Db 841 CGTGTTCGCCCAAGGATGAGAGGCTTCATCAGAGCCACACTTGTATGACATCTTG 900
QY 997 AACACATTAATATCTATCAACCGATCTCAACAGAGAGATATTAAGTCTGAGACACAG 1056
Db 901 AACACATTAATATCTATCAACCGATCTCAACAGAGAGATATTAAGTCTGAGACACAG 960
QY 1057 ATCATGCGCTCTCCAGTTGATGATGAGCGGAGCCGAGTTTAACTTCTCTCTATGAACT 1116

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Db      ATCATGGCTCTCCAGTGGATTGACGGCGGCCAGATTACCTTCCCTCTATGAACT 1020
Qy      961 ATGAGAAAGCGCGCTCCCAACAACGATCGTGTCTCAACAGGTCAGGGGTCTACAGA 1176
Db      1117 ATGAGAAAGCGCGCTCCCAACAACGATCGTGTCTCAACAGGTCAGGGGTCTACAGA 1080
Qy      1021 ATGAGAAAGCGCGCTCCCAACAACGATCGTGTCTCAACAGGTCAGGGGTCTACAGA 1236
Db      1177 ACCTTGTCTTCCACCTTGTACAGAAAGACCTTCAATCGGTATCAACACAGCAACTT 1236
Qy      1081 ACCTTGTCTTCCACCTTGTACAGAAAGACCTTCAATCGGTATCAACACAGCAACTT 1140
Db      1237 TCCGTTCTTGAACGAAACAGAGTTGGCTATGAAACCTTCTTAACCTGCTGTT 1236
Qy      1141 TCCGTTCTTGAACGAAACAGAGTTGGCTATGAAACCTTCTTAACCTGCTGTT 1200
Db      1297 TACGAAAGAGCGGAACCGTTGATTCTCTGAGACGAAATCCACACAGAACAAATGTG 1356
Qy      1201 TACGAAAGAGCGGAACCGTTGATTCTCTGAGACGAAATCCACACAGAACAAATGTG 1280
Db      1357 CCACCCAGGCAAGATTCTCCACAGGTTGAGCCACGTCATGTTCCGTTCCGATTC 1416
Qy      1261 CCACCCAGGCAAGATTCTCCACAGGTTGAGCCACGTCATGTTCCGTTCCGATTC 1320
Db      1417 AGCAACAGTTCGTCAGCATCATCAGAGCTCCATGTTCTCATGAGATTCTGATGCT 1476
Qy      1321 AGCAACAGTTCGTCAGCATCATCAGAGCTCCATGTTCTCTTGATTCACCGTATGCT 1380
Db      1477 GAGTTCAACATATCATCTCTTCCCTCAATTCACCAATCCCATTTGACCAAGCTACT 1536
Qy      1381 GAGTTCAACATATCATCTCTTCCCTCAATTCACCAATCCCATTTGACCAAGCTACT 1437
Db      1537 AACCTTGATCTGAAATCTTGTCTGTGAAAGAACAGGCTTCACAGAGGTGATATCTT 1596
Qy      1438 AACCTTCTCTTCAACGTTCTGTCTGATTCACAGGACAGGATTCACGTGAGACTCTGTT 1497
Db      1597 AGA 1599
Qy      1498 AGA 1500

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RESULT 6

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US-10-102-469-11
; Sequence 11, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT APPLICATION NUMBER: US/10/102,469
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 11
; LENGTH: 3534
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic structural gene encoding an insecticidal protein derive
; NAME/KEY: CDS
; LOCATION: (1)..(3534)
; OTHER INFORMATION:
US-10-102-469-11

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Query Match 50.6%; Score 1411.8; DB 12; Length 3534;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1453; Conservative 0; Mismatches 47; Indels 3; Gaps 1;
Qy      97 ATGACAAACAACCCAAACATCAACGATTCGATTCATACAACTGCTGAGTAACCCGAA 156
Db      1 ATGACAAACAACCCAAACATCAACGATTCGATTCATACAACTGCTGAGTAACCCGAA 60
Qy      157 GTTGAATGACTGGTGGAGAACGATTAAGAACCGGTATACACTCCATCGACATCTCTTG 216
Db      61 GTTGAATGACTGGTGGAGAACGATTAAGAACCGGTATACACTCCATCGACATCTCTTG 120
Qy      217 TCCCTTGAACAGATTTCCTGCTCAGGAGTTCGTGTCAGTGTGCTGTTCTTGGACTA 276
Db      121 TCCCTTGAACAGATTTCCTGCTCAGGAGTTCGTGTCAGTGTGCTGTTCTTGGACTA 180
Qy      277 GTTGAATCAATCTGAGGATTCCTTGTGTCATCTCAATGGAGTGTGATTCCTGTCGAATT 336
Db      181 GTTGAATCAATCTGAGGATTCCTTGTGTCATCTCAATGGAGTGTGATTCCTGTCGAATT 240
Qy      337 GAGCAGTTGATCAACACAGAGATGGAAGATTCGCCAGAAACAGGCATCTAGTTG 396
Db      241 GAGCAGTTGATCAACACAGAGATGGAAGATTCGCCAGAAACAGGCATCTAGTTG 300
Qy      397 GAAAGATTGAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGAGTGGAAACCGAT 456
Db      301 GAAAGATTGAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGAGTGGAAACCGAT 360
Qy      457 CCTACTAACCCAGCTCTCCGAGAGAAATGGTATTCATCAACGATCAAGAGGCC 516
Db      361 CCTACTAACCCAGCTCTCCGAGAGAAATGGTATTCATCAACGATCAAGAGGCC 420
Qy      517 TTGACCAAGCTATCCCATTTGTCAGTCCAGAACTCAAGTTCCTCTTCTGCTG 576
Db      421 TTGACCAAGCTATCCCATTTGTCAGTCCAGAACTCAAGTTCCTCTTCTGCTG 480
Qy      577 TACGTTCAAGCAGCTAATCTTCACTCAGCGTGTGAGAGCTTACGCTGTTGGCAA 636
Db      481 TACGTTCAAGCAGCTAATCTTCACTCAGCGTGTGAGAGCTTACGCTGTTGGCAA 540
Qy      637 AGTGGGATTCGATTCGTCGAACCATCAATAGCCGTTTACAGACCTTACAGCTGAT 696
Db      541 AGTGGGATTCGATTCGTCGAACCATCAATAGCCGTTTACAGACCTTACAGCTGAT 600
Qy      697 GGAACCTACACGACACGAGCTGTTGTTGTTAACAACACTGCTGAGAGCTGTGAGGT 756
Db      601 GGAACCTACACGACACGAGCTGTTGTTGTTAACAACACTGCTGAGAGCTGTGAGGT 660
Qy      757 CCTGATTTAGAGATTGATTAGATACCAACGATTCAGAGAGATTCAGCTTCAAGTT 816
Db      661 CCTGATTTAGAGATTGATTAGATACCAACGATTCAGAGAGATTCAGCTTCAAGTT 720
Qy      817 TTGACATTTGCTCTCTTCCGAACTATGACCTCCGAACCTTCCATCCGTACAGT 876
Db      721 TTGACATTTGCTCTCTTCCGAACTATGACCTCCGAACCTTCCATCCGTACAGT 780
Qy      877 TCCCAACTTACAGAGAAATCTATTAACCAAGTTCTTGAACCTTGAACCTGAGCTTC 936
Db      781 TCCCAACTTACAGAGAAATCTATTAACCAAGTTCTTGAACCTTGAACCTGAGCTTC 840
Qy      937 CGTGCTTGCCTCAAGGATTCGAAGGCTTCATCAGAGCCCACTTATGAGCAATCTTG 996
Db      841 CGTGCTTGCCTCAAGGATTCGAAGGCTTCATCAGAGCCCACTTATGAGCAATCTTG 900
Qy      997 AACGCAATATATATATACAGAGTCTCAGAGAGAGATTAATGATGACATCTTG 1056
Db      901 AACGCAATATATATATACAGAGTCTCAGAGAGAGATTAATGATGACATCTTG 960
Qy      1057 ATCATGGCTCTCCAGTTGGAATTCAGCGGCGCGAGTTTACCTTCTCTATGAACT 1116
Db      961 ATCATGGCTCTCCAGTTGGAATTCAGCGGCGCGAGTTTACCTTCTCTATGAACT 1020

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QY 1177 ACCTGTCTTCACCTTGTACAGAGACCCCTTCAATATCGGTATCAACACCAACTT 1236
 Db 1081 ACCTGTCTTCACCTTGTACAGAGACCCCTTCAATATCGGTATCAACACCAACTT 1140
 QY 1237 TCCGTTCTTGACGGAACGAGTTCGGCTATAGAACTCTTCTTAATCTTCCCTTCTT 1296
 Db 1141 TCCGTTCTTGACGGAACGAGTTCGGCTATAGAACTCTTCTTAATCTTCCCTTCTT 1200
 QY 1297 TACAGAAAGACGGGACCGGTGATTCCTTGACGGAATCCACCAAGAACAAATGTG 1356
 Db 1201 TACAGAAAGACGGGACCGGTGATTCCTTGACGGAATCCACCAAGAACAAATGTG 1260
 QY 1357 CCACCCAGGCAAGGATTCCTCCACAGGTTGAGCCAGTGTCCATGTTCCGTTCCGATTC 1416
 Db 1261 CCACCCAGGCAAGGATTCCTCCACAGGTTGAGCCAGTGTCCATGTTCCGTTCCGATTC 1320
 QY 1417 AGCAACAGTTCCTTGACGATATGACAGACTCTCTATGTTCTCATGATTCATCGTAGTCT 1476
 Db 1321 AGCAACAGTTCCTTGACGATATGACAGACTCTCTATGTTCTCTTGATATCACCGTAGTCT 1380
 QY 1477 GAGTTCAACATATCATCTCTTCTCTCAAAATCAACCAATCCCATTTGACCAAGTCTACT 1536
 Db 1381 GAGTTCAACATATCATCTCTCTCGATATGATTAATCTCAAAATCCCTGACGTGAAG---GGA 1437
 QY 1537 AACCTTGATCTGGAACCTTCTGTCTGGAAGAGACCGGCTTACAGAGGTGATATTTCTT 1596
 Db 1438 AACCTTCTCTCAACGGTTCTGTCTATTCAGAGACGAGATTCACTGTGTGAGACCTCTCTT 1497
 QY 1597 AGA 1599
 Db 1498 AGA 1500
 RESULT 8
 US-10-102-469-5
 ; Sequence 5, Application US/10102469
 ; Publication No. US20030192078A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischhoff, David A.
 ; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
 ; FILE REFERENCE: 38-21 (13553) B
 ; CURRENT APPLICATION NUMBER: US/10/102,469
 ; PRIOR FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: 08/434,105
 ; PRIOR FILING DATE: 1995-05-03
 ; PRIOR APPLICATION NUMBER: 07/959,506
 ; PRIOR FILING DATE: 1992-10-09
 ; PRIOR APPLICATION NUMBER: 07/476,661
 ; PRIOR FILING DATE: 1990-02-12
 ; PRIOR APPLICATION NUMBER: 07/315,355
 ; PRIOR FILING DATE: 1989-02-24
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 5
 ; LENGTH: 1767
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic structural gene encoding an insecticidal protein derive
 ; OTHER INFORMATION: d from B.t.k. HD-73
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(1767)
 ; OTHER INFORMATION:
 US-10-102-469-5
 Query Match 47.7%; Score 1328.8; DB 12; Length 1767;
 Best Local Similarity 96.5%; Pred. No. 0;
 Matches 1370; Conservative 0; Mismatches 47; Indels 3; Gaps 1;
 QY 180 CATTGAACCGGTACACTCCATGCATCTCTTCTTGTGACACAGTTTCTGTCTAG 239

Db 6 CATTGAACCGGTACACTCCATGCATCTCTTCTTGTGACACAGTTTCTGTCTAG 65
 QY 240 CGAGTTGTCGACAGTGTCTGGTTCGTTCTCGAGTATGATCATCTGTGGGATATCTT 299
 Db 66 CGAGTTGTCGACAGTGTCTGGTTCGTTCTCGAGTATGATCATCTGTGGGATATCTT 125
 QY 300 TGGTCCATCTCAATGAGATGATCTCTGTGTGCAATTTGACAGTTGATCAACAGAGAT 359
 Db 126 TGGTCCATCTCAATGAGATGATCTCTGTGTGCAATTTGACAGTTGATCAACAGAGAT 185
 QY 360 CGAAGATTCGCCAGAGAACAGGCAATCTCTAGTTGGGAAGATTGAGCAATCTTCA 419
 Db 186 CGAAGATTCGCCAGAGAACAGGCAATCTCTAGTTGGGAAGATTGAGCAATCTTCA 245
 QY 420 AATCTATGACAGAGACTTTCAGAGAGTGGGAAGCCGATCTTACTAACCCAGCTTCCGGA 479
 Db 246 AATCTATGACAGAGACTTTCAGAGAGTGGGAAGCCGATCTTACTAACCCAGCTTCCGGA 305
 QY 480 GGAATGCGTATTCATTCATTCACGATGAACAGCGCTTGTGACACAGCTATCCCATTTGT 539
 Db 306 GGAATGCGTATTCATTCATTCACGATGAACAGCGCTTGTGACACAGCTATCCCATTTGT 365
 QY 540 CGGAGTCCAGAACTACCAAGTTCCTCTCTGTCGTTAGGTTCAAGCAGTATCTTCA 599
 Db 366 CGGAGTCCAGAACTACCAAGTTCCTCTCTGTCGTTAGGTTCAAGCAGTATCTTCA 425
 QY 600 CCTGAGCGTCTTCGAGACGTTAGCGTGTGGAAGGAGGAGATTCGATGTGCAAC 659
 Db 426 CCTGAGCGTCTTCGAGACGTTAGCGTGTGGAAGGAGGAGATTCGATGTGCAAC 485
 QY 660 CATCAATAGCGTTTACCAACGACCTTACTAGCTGATTTGAAATCTAACCCGACAGCTGT 719
 Db 486 CATCAATAGCGTTTACCAACGACCTTACTAGCTGATTTGAAATCTAACCCGACAGCTGT 545
 QY 720 TCGTTGGTACAAACCTGGCTTGGAGCGTGTGGGGTCTCGAATCTGAGATTGAGATTAG 779
 Db 546 TCGTTGGTACAAACCTGGCTTGGAGCGTGTGGGGTCTCGAATCTGAGATTGAGATTAG 605
 QY 780 ATACAAACGAGTTCAGAGAGAGATTAACCTTCACAGTTTGGACATTTGTCTCTTCCC 839
 Db 606 ATACAAACGAGTTCAGAGAGAGATTAACCTTCACAGTTTGGACATTTGTCTCTTCCC 665
 QY 840 GAACTATGACTTCCGAACTTACCTTATCCGTACAGTGTCCCACTTACAGAGAAATCTA 899
 Db 666 GAACTATGACTTCCGAACTTACCTTATCCGTACAGTGTCCCACTTACAGAGAAATCTA 725
 QY 900 TACTAACCCAGTTCAGAGAGATTAACCTTCACAGTTTGGAGTTCGTCGCAAGGATGGA 959
 Db 726 TACTAACCCAGTTCAGAGAGATTAACCTTCACAGTTTGGAGTTCGTCGCAAGGATGGA 785
 QY 960 AGGCTCATCAGAGACCCACACTTATGATGATGATGATGATGATGATGATGATGATGATG 1019
 Db 786 AGGCTCATCAGAGACCCACACTTATGATGATGATGATGATGATGATGATGATGATGATG 845
 QY 1020 TGGTCAAGAGAGAGATTAATGAGTGTGACACCAAGATCATGAGCTTCTCCAGTTGATT 1079
 Db 846 TGGTCAAGAGAGAGATTAATGAGTGTGACACCAAGATCATGAGCTTCTCCAGTTGATT 905
 QY 1080 CAGGGGGGCGAGTTTACCTTCTCTCTATGAACTTGGGAAAGCGCGTCCACACA 1139
 Db 906 CAGGGGGGCGAGTTTACCTTCTCTCTATGAACTTGGGAAAGCGCGTCCACACA 965
 QY 1140 ACGTATCGTTCCTCAACTAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 1199
 Db 966 ACGTATCGTTCCTCAACTAGGTGATGATGATGATGATGATGATGATGATGATGATGATG 1025
 QY 1200 AAGACCTTCAATATCGGTATCAACACAGCAACTTTCGTTCTTGACGGAACAGATT 1259
 Db 1026 AAGACCTTCAATATCGGTATCAACACAGCAACTTTCGTTCTTGACGGAACAGATT 1085
 QY 1260 CGCCTATGAAACCTTCTTAATCTGCAATCGCTGTTCAGAAAGAGCGGAACGCTTGA 1319

Db 1086 GCGCTATGGAACCTCTTTAACTTGCCATCCGCTGTTTACAGAAAAGCGGAACCGTTGA 1145
Qy 1320 TTCCTTGGACGAAATCCCAACGACAGAAACAAATGTGCAACCCAGGACGATTTCTCCCA 1379
Db 1146 TTCCTTGGACGAAATCCCAACGACAGAAACAAATGTGCAACCCAGGACGATTTCTCCCA 1205
Qy 1380 CAGGTGAGCCACGCTGCTTCCATGTTCCGTTCCGATTCAGCAACGTTCCGTGAGCATCAT 1439
Db 1206 CAGGTGAGCCACGCTGCTTCCATGTTCCGTTCCGATTCAGCAACGTTCCGTGAGCATCAT 1265
Qy 1440 CAGAGCTCCTATGTTCTTCAATGATTCATGCTGAGTCCGATTCAGCAATATCATTCCTTC 1499
Db 1266 CAGAGCTCCTATGTTCTTCAATGATTCATGCTGAGTCCGATTCAGCAATATCATTCCTTC 1325
Qy 1500 CTCCTCAATCACCACCAATCCCATTTGACCAAGTCTACTACCTTGATCTGGAACCTTCTGT 1559
Db 1326 CGATAGTATTAATCAATCCCTGCAAGTGAAG---GGAACCTTCTCTTCAACGGTTCTGT 1382
Qy 1560 CGTGAAAGGACCGAGCTTCACAGAGGTGATTTCTTGA 1599
Db 1383 CATTTCAAGACCGAGATTCACCTGTGTGAGACCTCGTTAGA 1422

RESULT 9

US-09-756-643-1
Sequence 1, Application US/09756643
Patent No. US20010026939A1
GENERAL INFORMATION:

APPLICANT: Rice, Douglas
APPLICANT: Carozzi, Nadine
APPLICANT: Anderson, David
APPLICANT: Rajasekaran, Kanniah
APPLICANT: Rangan, Thirumale
APPLICANT: Yenofsky, Richard
APPLICANT: Lotstein, Richard
APPLICANT: De Pramond, Annick
TITLE OF INVENTION: Insecticidal Cotton Plant Cells
FILE REFERENCE: S-16768E
CURRENT APPLICATION NUMBER: US/09/756,643
CURRENT FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 08/216,697
PRIOR FILING DATE: 1994-03-28
PRIOR APPLICATION NUMBER: 07/759,969
PRIOR FILING DATE: 1991-09-16
PRIOR APPLICATION NUMBER: 07/274,452
PRIOR FILING DATE: 1988-11-18
PRIOR APPLICATION NUMBER: 07/122,109
PRIOR FILING DATE: 1987-11-18
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4360
TYPE: DNA
ORGANISM: Bacillus thuringiensis
FEATURE:
NAME/KEY: CDS
LOCATION: (156)..(3623)
US-09-756-643-1

Query Match 43.8%; Score 1220.4; DB 9; Length 4360;
Best Local Similarity 77.6%; Pred. No. 0;

Matches 1476; Conservative 0; Mismatches 426; Indels 0; Gaps 0;

Qy 39 AAAAAAACCCTATAATATTCGAGATTATTCATACCGTCCACCATCGGCGCGAGTCAAT 98
Db 98 AAAAAACGATTAATATCAATGAATGGTATCTTAATAAAGATGAGGTAACTTAT 157
Qy 99 GGACAAACAACCCAAACATCAACGAATGCAATTCATCAACAATGCTGAGTAACCCAGAAAT 158
Db 158 GGATTAACAATCCGAACATCAATGAATGCAATCTTAAATATGTTTAAAGTAACCTGAAGT 217
Qy 159 TGAATACTTGTGTGAGAAAGCATTTGAACCGGTTAACTCCCATGACATCTCCTTGT 218

Db 218 AGAAGTATTAGTGGAGAAAAGATAGAAACTGGTTACACCCCAATGCAATATTTCTGTCTC 277
Qy 219 CTGACACAGATTTCTGCTCAGCGATTCGTGCCAGGTGCTGGGTTCTGCTTCGGACATGT 278
Db 278 GCTAACGCAATTTCTTTGAGTGAATTTGTTCCGGGTGCTGGAATTTGTGTTAGGACATGT 337
Qy 279 TGACATATCTGGGGTATCTTTGGTCCATCTCAATGGGAATGCAATTTCTGTGCAAAATGA 338
Db 338 TGATATATATATGGGAAATTTTGGTCCCTCTCAATGGGAACGCAATTTCTTGAACAAATGA 397
Qy 339 GCAGTTATATCAACGAGGATTCGAAGTTCCGAGGAACCAAGGCAATCTCTAGATTGA 398
Db 398 ACAGTTATATTAACCAAGAAATAGAAATTCGCTAGGAACCAAGCAATTTCTAGATTGA 457
Qy 399 AGGATTGAGCAATCTTACCAATCTATGCAAGAGCTTCAGAGAGTGGGAAGCCGATCC 458
Db 458 AGGATTAAGCAATCTTATCAAAATTTACGAGAAATCTTTTAGAAGTGGGAAGCAATTC 517
Qy 459 TACTAACCCAGCTCTCCGAGGAATGCCATTCATTCACAGCAATGAACAGCGCTT 518
Db 518 TACTTAATCCAGCAATTAAGAAAGATGCCATTCATTCATTAACATGAACAGTGCCT 577
Qy 519 GACCAGAGCTATCCATTTGTTGCGAGTCCAGAACTACCAAGTTCTCTGTGCTGCTGA 578
Db 578 TACAACCGCTATTTCTCTTTTTCGAGTTCAAAATTAACAGTTCTCTTTTATCAGTATA 637
Qy 579 CGTTCAAGCACTAATCTTCACTCAGCGTCTTCGAGCGTTAGCGTGTGCGCAAG 638
Db 638 TGTTCAGGTCGAATTTACATTAATCATGATTTGAGAGATGTTTCAAGTGTGCAACAAAG 697
Qy 639 GTGGGATTCGATCTCTGCAACATCAATAGCCGTTTCAACGACCTTACTAGGCTGATTTG 698
Db 698 GTGGGATTTGATGCCCGCACTAATCAATAGCTGTTAATTAATTAATTAATTAATTAATTAAT 757
Qy 699 AAATTAACCGGACCGAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 758
Db 758 CAATTAATCAAGATATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 817
Qy 759 TGATTTAGAGATTGATTAATCAACCAAGTTGAGAGAGAAATTTGACCTCAGAGTTT 818
Db 818 GGATTTAGAGATTGATTAATCAATTAATCAATTAATTAATTAATTAATTAATTAATTAAT 877
Qy 819 GGAATGTTGTTCTCTTCCGAACTATGACTCCAGAACTCACTATCCGTACAGTGT 878
Db 878 AGATATGTTTCTCTATTTCCGAATTAATGAATGAACGATATCAATTCACAAAGTTTC 937
Qy 879 CCAACTTAACGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 938
Db 938 CCAATTAACGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 997
Qy 939 TGTGTTGCTCCAGATTCGAAGGCTCCATCAGAGCCACACTTGATGACATCTTGAA 998
Db 998 AGGCTCGGCTCAGGAGATTAAGAGAAATTAAGAGTCCATTTGATGATTAATTAATTAAT 1057
Qy 999 CAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1058
Db 1058 CAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1117
Qy 1059 CATGAGCTCTCAGTTGATTCAGCGGCGCGAGTTTACCTTCTCTCTATGAACTAT 1118
Db 1118 AATGAGCTCTCTGATGAGTTTTCGGGCGCGAGTTTACCTTCTCTCTATGAACTAT 1177
Qy 1178 GGAAGATCACTCCACAAACGATTTGTTGCTCACTAGGTAGGCGGTGTATGAAC 1237
Db 1237 GGAAGATCACTCCACAAACGATTTGTTGCTCACTAGGTAGGCGGTGTATGAAC 1237
Qy 1238 CTGCTCTGCACTTTGTCAGAAAGCCCTTGAATGCTTCAACCAACGAGCAATTC 1238
Db 1238 AATATGCTGCACTTTATTAATGAAGCCCTTGAATGCTTCAACCAACGAGCAATTC 1297
Qy 1239 GGTCTTGAAGGAAAGAGATTCGCTATGAAACCTCTTCAATGCTTGAACCTCGGTGTTA 1298
Db 1298 TGTCTTGAAGGAAAGATTCGCTATGAAACCTCTCTCAATGCTTGAACCTCGGTGTTA 1357

Db 361 CTTACTATCCAGATTAAAGAAAGAGATGCGTATTCTCAATTGATGATGAAACAGTCC 420
 Qy 517 TTGACCAAGCTATCCAGATTGTTGCGAGTCCAGAACTACCAAGTTCTCTGTCGCG 576
 Db 421 CTTACAAACCGGTATTCCTCTTTTGGAGATTCAAAATATCAAGTTCCCTTTTATCA 480
 Qy 577 TAGCTTCAAGCAGCTAATCTTCACTCAGCGTCTTGAGACGTTAGCGTTTGGGCA 636
 Db 481 TATGTTCAAGCTGCAAAATTTACATTTATCAAGTTTGAAGATGTTTCAAGTTGGA 540
 Qy 637 AGGTGGGGAATTCAGTGGTGAACCATATAGCGGTTTCAACGACCTTACTAGGCTGAT 696
 Db 541 AGGTGGGGAATTTGATGCGGACATCAATAGCTTATATATGATTTAACTAGGCTTAT 600
 Qy 697 GGAATCTACACGACCAAGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 756
 Db 601 GGCACATATACAGATCAATGCTGTACGCTGTACAAATCGGGAATTAGACGCTGAT 660
 Qy 757 CTTGATTTAGAGATTGGATTAGATACAAACGATTACAGAGAGAAATGACCTTCAAG 816
 Db 661 CCGGATTTCTAGAGATTGGATTAGATATCAATTTTGAAGAGATTTAACTAACTGTA 720
 Qy 817 TTGACATTTGCTCTCTCTCCGAACTATGACTCCGAACTTACCTATCCGTAAGCTG 876
 Db 721 TTGATATTCGTTCTCTATTTCCGAACTATGATAGTAAGTCCAAATTCGAAACGTT 780
 Qy 877 TCCCACTTACAGAGAAATCTATATCTAACCCAGTTCTTGAACTTTCGACGTTAGCT 936
 Db 781 TCCCAATTTAAAGAGAAATTTATCAAAACCAAGATTAGAAATTTTGAATGATGTT 840
 Qy 937 CGTGTCTTCCGCAAGGATGAAAGGCTCCATCAGAGCCCACTTGTATGACATCTTG 996
 Db 841 CGAGGCTCGGCTCAGGGGATGAAGAGATTTAGAGTCCCAATTTGATGATATCTT 900
 Qy 997 AACGCAATTAATCTATACAGGATGCTACAGAGAGATTTCTGCTGGAACACG 1056
 Db 901 AACGATTAACCACTATACGAGTCTATAGAGAGATTTATGCTCAGGGCATTA 960
 Qy 1057 ATCATGCGCTTCCAGTTGATTCAGCGGGCCGAGTTTACCTTCTCTATAGAACT 1116
 Db 961 ATATGCTTCTCCGTAGGGTTTCCGGGCCAGAAATTCATTTCCGCTATATGAACT 1020
 Qy 1117 ATGGAAACCGCGCTCCCAACAAACGATTCGTTGCTCACTAGAGTCAAGGTTCTACA 1176
 Db 1021 ATGGAAATGACGCTCCCAACAAACGATTCGTTGCTCACTAGAGTCAAGGTTCTACA 1080
 Qy 1177 ACCTGCTTCCACTTGTACAGAAAGACCTTCAATTCGCTATCAAAACAGAACTT 1236
 Db 1081 ACATTTATGCTCACTTATATAGAAACCTTTTAAATAGGATTAATATCAACACTTA 1140
 Qy 1237 TCCGTTCTTGAAGCAAGAGTTCGCTATGAAACCTTCTTAACTTCCATCCGCTGT 1296
 Db 1141 TCTGTTCTTGAAGCAAGATTTGCTTATGAAACCTCTCAAAATTTCCATCCGCTGTA 1200
 Qy 1297 TACGAAAGAGCGGAACCGTTGATTCCTTGAAGAAATCCACACAGAAACAATGTG 1356
 Db 1201 TACGAAAGAGCGGAACCGTAGATTGCTGATGAAATACCGCCACAGAAATCAACCTG 1260
 Qy 1357 CCACCCAGGCAAGATTCTCCACAGTTGAGCCAGCTGCTCATGTTCCGTTCCGAGTTC 1416
 Db 1261 CCACCTAGGCAAGATTGATCATGATTAAGCCAGTTTCAAGTTTCCGTTCCGAGTTC 1320
 Qy 1417 AGCAACAGTTCCGTAGAGCATCATGAGCTCTATGTTCTGATGATTCATCTGATGCT 1476
 Db 1321 AGTAAATAGTAGTAAGTAAATAGAGCTCTATGTTCTTGGATCATCTGATGCT 1380
 Qy 1477 GAGTTCAACATATATCTCTCTCTCAATCAACCAATCCCTTGAACCAAGCTACT 1536
 Db 1381 GAATTTAATATATATCTCTCTCAACCAATTTACAAATTAACCTTTAAACAAATCTACT 1440
 Qy 1537 AACCTTGATCTGAACCTTCTGCTGAAGAGACGAGCTTACAGAGAGTATATTTCTT 1596
 Db 1441 AATCTTGCTCTGAACCTTCTGCTTAAAGACCAAGATTTTACAGAGAGATATTTCTT 1500

Qy 1597 AGAAGACTTCTCTGCGCCAGATTAGACCCCTCAGAGTTAACTACTGCACCACTTCT 1656
 Db 1501 CGAAGACTTCACTGCGCCAGATTATCAACCTTAAAGATTAATATCTAGCACCATTATCA 1560
 Qy 1657 CAAAGATATGCTGCAGAGATTGCTTACAGATCTTACCACTAACTTGAATCCACCTCC 1716
 Db 1561 CAAAGATATGCTGCAGAGATTGCTTACAGATCTTACCACTAACTTGAATCTATCAATCA 1620
 Qy 1717 ATCAGCAGAGGCTTAACTCAATCAGAGGTTACTTCCGCAACCAATGTCAGCGCAGCAAC 1776
 Db 1621 ATTGACGGAAGACCTTAACTTAACTCAGGGAATTTTTCACCACTAATGATAGTGGAGTAT 1680
 Qy 1777 TTGCAATCGGACGCTTCAAGACCGTCTTCACTAATCTCTTCAACTTCTTCAACGA 1836
 Db 1681 TTACAGTCCGGAAGCTTTAGGAGCTGATGATTTTACTCTCCGTTTAACTTTCAAAATGA 1740
 Qy 1837 TCAAGCTTTTACCTTACGCTCAATGCTGTTCAATCTGCAATGGAATGATCATTTGAC 1896
 Db 1741 TCAAGTGTATTTAGTTAGTCTCATGCTTCAATTCAGGCAATGGAATGATATGAT 1800
 Qy 1897 CGATTGATTTTGTGCTGCGCAGATTACCTTCCAGGCTGAGTA 1940
 Db 1801 CGAATTGAATTTGTTCCGGCAGAGTAACTTTGAGGCAAGATA 1844

 RESULT 11
 US-10-035-060-7
 : Sequence 7, Application US/10035060
 : Publication No. US20030040619A1
 : GENERAL INFORMATION:
 : APPLICANT: Edwards, David
 : APPLICANT: Wong, Siu-Yin
 : APPLICANT: Herrnstadt, Corinna
 : APPLICANT: Milcox, Edward
 : TITLE OF INVENTION: Process For Altering the Host Range Or Increasing The
 : TITLE OF INVENTION: Toxicity Of
 : TITLE OF INVENTION: Bacillus Thuringiensis Lepidoteran Toxins, and Recombinant DNA
 : FILE REFERENCE: M121FDF3D1
 : CURRENT APPLICATION NUMBER: US/10/035, 060
 : PRIOR FILING DATE: 2001-12-27
 : PRIOR APPLICATION NUMBER: 09/405, 788
 : PRIOR FILING DATE: 1999-09-27
 : PRIOR APPLICATION NUMBER: US 08/580, 781
 : PRIOR FILING DATE: 1995-12-29
 : PRIOR APPLICATION NUMBER: US 08/420, 615
 : PRIOR FILING DATE: 1995-04-10
 : PRIOR APPLICATION NUMBER: US 08/097, 808
 : PRIOR FILING DATE: 1993-07-27
 : PRIOR APPLICATION NUMBER: US 07/980, 128
 : PRIOR FILING DATE: 1992-11-23
 : PRIOR APPLICATION NUMBER: US 07/803, 920
 : PRIOR FILING DATE: 1991-12-06
 : PRIOR APPLICATION NUMBER: US 07/356, 599
 : PRIOR FILING DATE: 1989-05-24
 : PRIOR APPLICATION NUMBER: US 06/904, 572
 : PRIOR FILING DATE: 1986-09-05
 : PRIOR APPLICATION NUMBER: US 06/808, 129
 : PRIOR FILING DATE: 1985-12-12
 : NUMBER OF SEQ ID NOS: 9
 : SOFTWARE: PatentIn version 3.0
 : SEQ ID NO 7
 : LENGTH: 3531
 : TYPE: DNA
 : ORGANISM: Bacillus Thuringiensis
 US-10-035-060-7

 Query Match 43.0%, Score 1197.6, DB 14, Length 3531,
 Best Local Similarity 78.1%, Pred. No. 0,
 Matches 1440, Conservative 0, Mismatches 404, Indels 0, Gaps 0:
 Qy 97 ATGACAAACCAACCAATCAAGAAATGCAATTCATATCAACTGCTTGATTAACCCAGAA 156

Db 1 ATGATATACATCCGAATCATATGAATGATTCCTTATATTTGTTAAGTAACCTGAA 60
 Oy GTTGAAGACTTGGTGGAGAACGATTTGAACCGGTTACACTCCCATGACATCCCTGG 216
 Db 61 GTAGAAGATTAGGGGAGAAAGAAATGAACCTGGTTACACCCCAATGATATTTCTTG 120
 Oy TCTTGAACACAGTTTGTGCTCAGCGAGTTCTGCGCAGGTGCTGGGTTGTTCTCGACTA 276
 Db 121 TCGCTAACGCAATTTCTTTAGTGAATTTGTTCCCGGTGCTGATTTGTGTAGACTA 180
 Oy GTTGAATCATCTGGGGTATCTTTGTGCTCATCTCAATGGATTCATTTCTGTGCAATTT 336
 Db 181 GTTATATATATGGGGAATTTTGTGCTCTCATGGGAGCGCATTTCTGTACAAATTT 240
 Oy GAGAGTTGATCAACCAAGATCGAAGATTCGCGAGAAACGAGCCATCTAGAGTG 396
 Db 241 GAACAGTTAATTAACCAAGATGAGAAATTCGCTAGGAACCAAGCCATTTCTAGATTA 300
 Oy GAAGGATTGACCAATCTCTACCAATCTATGACAGAGCTTCAGAGAGTGGAAAGCCGAT 456
 Db 301 GAAGGACTTAAGCAATCTTTATCAATTTACGAGAACTTTTAGAGAGTGGAAAGCAAT 360
 Oy CTTACTAACCAAGCTCTCCGAGAGAAATGCGTATTCATTTCAACGACATGAACGCC 516
 Db 361 CCTACTAATCCAGACTTAAGAGAGAGATGCGTATTCATTTCAATGACATGAACAGTCC 420
 Oy TTGACCAAGCTATCCCATTTGTGCGATCCAGAACTCAAGTTCCTCTGTGCGGTG 576
 Db 421 CTTAACACCGATTCCTCTTTTGCAAGTCAAAATTAACAAATTCCTTTTATCAAGTA 480
 Oy TACGTTCAAGAGCTAATCTTCACTCAGCGTCTTCGAGACGTTAGCGTGTGGGCA 636
 Db 481 TATGTTCAAGCTGCAATTTACATTTATCAAGTTTGAAGAGATTTTCAAGTGTGGACA 540
 Oy AGTGGGAGATTCGATGCTGCAACATCAATAGCCGTTCAACGACCTTACTAGCGTAT 696
 Db 541 AGTGGGAGATTTGATGCGCGCACTATCAATAGTCTTAAATGATTTAACTAGCGTATTT 600
 Oy GGAACCTACACCGACCAAGCTGTTGTTGTAACAACCTGCTGAGAGGTCTGGGAT 756
 Db 601 GGAACCTACACAGATTTAGCTGTACGCTGTGTAACAACCTGCTGAGAGGTCTGGGAT 660
 Oy CCGTATCTAGAGATTTGATGATTAACAACAGTTCAAGAGAAATGACCTCTCAAGTT 816
 Db 661 CCGGATCTAGAGATTTGGGTAAGTATATCAATTTAGAGAGAAATTAACAATTAAGTAT 720
 Oy TTGACATTTGTGCTCTCTCCGAACTATGATCTCCAGAACTTACCCTATCCGTACAGTG 876
 Db 721 TTAGATATCGTTGCTCTGTTCCCGAATTAATGATAGTAAGATTCGAATTCGAACAGTT 780
 Oy TCCCAACTTACCGAGAAATCTATCTAACCCAGTTCTTGAACCTTGAAGCGGTAGCTTC 936
 Db 781 TCCCAATTAACAGAGAAATTTATACAAACCCAGATTTAGAAATTTTGTAGTGTGTTT 840
 Oy CGTGTCTTCCCAAGGATTCGAAGGCTTCATCAGAGCCCACTTGAATGACATCTTG 996
 Db 841 CGAGCTCGGCTCAGGGCATAGAGAGATTTAGAGAGTCCACATTTGATGATTAATCTT 900
 Oy AAGACATTAATCTATCTACACCGATGCTCAACAGAGAGATTTACTGTGTGAGAACAG 1056
 Db 901 AAGACATTAATCACTATACGAGATGCTCAAAAGGGAATATTTATTTGTGTCAGGGCATCAA 960
 Oy ATCATGAGCTCTCCAGTTGATTTCAAGCGGGCCGAGTTTACCTTCTCTCTATGAACT 1116
 Db 961 ATTAATGAGCTCTCTGTAGGGTTTTCGGGCCAGAAATTAATCTTTCCGTATATGAACT 1020
 Oy ATGGGAAAGCGCGCTCCACAAACGATCTGTTGCTCAACTAGTCAAGGCTGTTACAGA 1176
 Db 1021 ATGGGAAATGCAAGCTCCACAAACGATTTGTTGCTCAACTAGTCAAGGCGCTGATAGA 1080
 Oy ACCTGTCTTCAACCTTGTACGAAGAACCTTCAATATGCGTATCAACAACGAACTT 1236

Db 1081 ACATTAATCGTCCACTTTATATAGAACCTTTTATATATAGGATTAATTAACAACATA 1140
 Oy TCGGTTCTTGAACGAAACAGAGTTTGCCTATAGGAACCTTTCTTAATCTTCCATCGCTGT 1296
 Db 1141 TCGTCTTGAACGGAACAGAGTTTGTATAGGAACCTTCAAAATTTGCGATCGCGTGA 1200
 Oy TACGAAAGAGCGGAACCGTTGATTTCTTGTGAGAAATCCCAACAGAAACAAATGTG 1356
 Db 1201 TACGAAAGAGCGGAACGATGATTCGCTGATGAAATACCGCAAGAAATTAACAGTGT 1260
 Oy CCACCCAGGAAGATTTCTCCCAAGGTTAGGCAAGTGTCCATGTTCCGTTCCGATTC 1416
 Db 1261 CCACCTAGGCAAGATTTAGTCATGATTAAGCCATGTTCAATGTTTCTGTCAGGCTTT 1320
 Oy AGCAACAGTTCCGAGACATCATAGAGCTCTATGTTCTCATGATTTCAATCTGATGTCT 1476
 Db 1321 AGTAATGATGATGATTAATTAAGAGCTCAACGTTTCTTGGAGCATCCGAGTGT 1380
 Oy GAGTTCAACAAATATCATTTCTTCTCTCTCAAAATCAACCAATTCATGACCAAGTCTA 1536
 Db 1381 GAATTTAATTAATTAATTTCTTCTCATCAAAATTAACAAATACCTTTAAACAAATCTA 1440
 Oy AACCTGATCTGGAATCTGTTGTGAAAGGACCAAGCTTCAAGAGGATGATTTCTT 1596
 Db 1441 AATCTGCTGTGAACTTCTGTGTTTAAAGGACCAAGATTTACAGAGAGATATTTCTT 1500
 Oy AGAAGACTTCTCCTGCGCAGATTTAGCAACCTCAGAGTTAATCATCTGCAACACTTCT 1656
 Db 1501 CGAAGACTTCACTGCGCAGATTTCAACCTTAAGAGTAATATATCTGCAACATTA 1560
 Oy CAAGATATGCTGTGAGATTTGTTAGCATCTCAACATACTTCAATTTCAACACTCTC 1716
 Db 1561 CAAGATATCGGTAAGAAATTCGCTAGCTTCTCAATTTCAATTTCAATTTCAATTTCA 1620
 Oy ATGACGGAAGGCTTATCAATCAGGATTAATCTTCCGCAACCATGTAAGGCGAGCAAC 1776
 Db 1621 ATTAACGGAACCTTATTAACAGGATTAATTTTCAAGCAATTAAGATGAGGAGTAA 1680
 Oy TTGCATTCGCGACCTTCAGAACCGTGTTCCTACTCTCTTCAACTTCTTCAACGGA 1836
 Db 1681 TTACAGTCGGAACCTTTAGGACGTTAGGTTTACTACTCGTTTCACTTTCAATGGA 1740
 Oy TCAAGCTTTTCAACCTTTAGGCTCATGCTCTTCAATTTCAAGCAATGAAGTTTATATAG 1896
 Db 1741 TCAAGCTTTTCAAGCTTTAGGCTCATGCTCTTCAATTTCAAGCAATGAAGTTTATATAG 1800
 Oy CGTATGAGTTTGTGCTGCGCGAGATTAACCTTGAAGGCTGAGTA 1940
 Db 1801 CGAATGAAATTTGTTCCGCGAGAGTAACCTTTGAGCGAGATA 1844

RESULT 12
 US-10-035-060-3
 ; Sequence 3, Application US/10035060
 ; Publication No. US20030040619A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edwards, David
 ; APPLICANT: Wong, Siu-Yin
 ; APPLICANT: Herrnsfeldt, Corinna
 ; APPLICANT: Wilcox, Edward
 ; TITLE OF INVENTION: Process For Altering the Host Range Or Increasing The
 ; TITLE OF INVENTION: Toxicity Of
 ; TITLE OF INVENTION: Bacillus Thuringiensis Lepidopteran Toxins, and Recombinant DNA
 ; FILE REFERENCE: M12C1DF3D1
 ; CURRENT APPLICATION NUMBER: US/10/035,060
 ; CURRENT FILING DATE: 2001-12-27
 ; PRIOR APPLICATION NUMBER: 09/405,788
 ; PRIOR FILING DATE: 1999-09-27
 ; PRIOR APPLICATION NUMBER: US 08/580,781
 ; PRIOR FILING DATE: 1995-12-29
 ; PRIOR APPLICATION NUMBER: US 08/420,615
 ; PRIOR FILING DATE: 1995-04-10

PRIOR APPLICATION NUMBER: US 08/097,808
 PRIOR FILING DATE: 1993-07-27
 PRIOR APPLICATION NUMBER: US 07/980,128
 PRIOR FILING DATE: 1992-11-23
 PRIOR APPLICATION NUMBER: US 07/803,920
 PRIOR FILING DATE: 1991-12-06
 PRIOR APPLICATION NUMBER: US 07/356,599
 PRIOR FILING DATE: 1989-05-24
 PRIOR APPLICATION NUMBER: US 06/904,572
 PRIOR FILING DATE: 1986-09-05
 PRIOR APPLICATION NUMBER: US 06/808,129
 PRIOR FILING DATE: 1985-12-12
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO: 3
 LENGTH: 3531
 TYPE: DNA
 ORGANISM: *Bacillus thuringiensis*
 US-10-035-060-3

Query Match 42.8%; Score 1194.4; DB 14; Length 3531;
 Best Local Similarity 78.0%; Pred. No. 0;
 Matches 1438; Conservative 0; Mismatches 406; Indels 0; Gaps 0;

97 ATGACAAACAAACCAACATCAAGATGATCCCATCAACTGCTGAGTAACCCAGAA 156
 1 ATGAGATAACATCCGAAACATCAATGATGATCCCTTATATGTTTAAATGTAACCCGAA 60
 157 GTTAAGACTTGTGGAGAAAGCATGAAACCGTTTCACTCCCATGACATCTCCCTG 216
 61 GTAGAATATTAGGAGAAAGATAGAACTGGTTACACCCCAATGATATATTTCTTG 120
 217 TCCTTGACACAGTTTCTGCTCAGCAGATCGTGCCAGGTGCTGGTTGTTCTCGACTA 276
 121 TCGTAAACGATTTCTTTAGTGAATTTGTTCCGGTGCTGATTTGTTAGACTA 180
 277 GTTGCATCATCTGGGATATCTTTGCTCATCTCAATGGATTCGATTTCTGGTGAATT 336
 181 GTTGAATATATAGGGAATTTTGGTCCCTCTCAATGGAGCGCATTTCTGTCAAAATT 240
 337 GAGCAGTGAATCAACCAAGAGATGAGATTCGCGCAGAAACCGCCATCTTAGGTTG 396
 241 GAACGTTAATTAACCAAGATAGAAATTCGTTAGAAACCAAGCCATTTCTAGATTA 300
 397 GAAGGATTAGCAATCTCTACCAATCTATGACAGAGCTTCAGAGATGGAAAGCCGAT 456
 301 GAAGGACTAAGCAATCTTTATCAATTTACGAGAACTTTTAGAGATGGGAAGCAGAT 360
 457 CCTACTAACCAAGCTCTCCGCGAGAAATGCGTATTTCAATTCAGACATGACAGCGCC 516
 361 CCTACTAATCCAGCAATTAAGAGAGATGCGTATTTCAATTCAGACATGACAGTCC 420
 517 TTGACCAAGGCTCCCATGTTGGCAGTCCAGAACTCAAGTTCCTCTGTGCGGTG 576
 421 CTTAACACCGATTTCTCTTTTGGAGTTCAAAATTTCAAGTTCTCTTTTATCAGTA 480
 577 TACGTTCAAGAGCTAATCTTCACTCAGCGTCTTCGAGACGTTAGCGTGTGGGCA 636
 481 TATGTTAAGCTGCAAAATTTACATTTACAGTTTGAAGAGATTTTCAAGTGTGGACA 540
 637 AGGTGGGATTCGATGCTGCAACATCAATAGCCGTTTCAAGACCTTACTAGGTGATT 696
 541 AGGTGGGATTTGAAGCGCGCACTATCAATAGTCTTATATGATTTAACTAGGCTTATT 600
 697 GGAATCTACACGACGACGAGTGTGTTGCTGACACATGCGCTTGAGAGGTGCTGGGT 756
 601 GGCACCTATACAGATTAAGCTATAGCTGTGACAAATAGCGGATTTAGAACGTATAGGGA 660
 757 CCTGATTTCTAGAGATTGATTAATCAACAGATTCAAGAGAAATTGACCTCTCAAGTT 816
 661 CCGGATTTCTAGAGATTGGGTAGGTATATCAATTTAGAGAGAAATTAACTAATCTGTA 720
 817 TTGGACATTTGTCTCTCTCCGGAATATGACTCCAGAACTACCTATCCGTACAGTG 876

721 TTAGATATGCTGCTCTGTTCCGAATTATAGATAGAAAGATATCAATTCGAACGTT 780
 877 TCCCAACTTACAGAGAAATCTATTAACCCAGTTCTTGAGAACTTGAAGGTGCTTC 936
 781 TCCCAATTAACAGAGAAATTTATCAAAACCGATTTAGAAATTTTGAATGGATTTT 840
 937 CGTGTTCGCGCCAGGATATGAAAGCTCCATCAGAGCCCACTTGAATGACATCTTG 996
 841 CGAGGCTCGCGCTAGGCGCATAGAAAGATTAAGGATGTCACATTTGATGATATCTT 900
 997 AACAGCATATCTATCAACCGATGCTCAGAGGAGATTAATAGGTCTGAGACACAG 1056
 901 AACAGTATTAACATCTATACGATGCTCATAGGGGTTATTTATTTGTTAGGCGATCA 960
 1057 ATCATGCTCTTCAGTTGATTCAGCGGCGCAGATTTACCTTCTCTATGAACT 1116
 961 ATATGCTCTCTCTGATAGGTTTGGGGCCGAATTCATTTCCGCTATATGAACT 1020
 1117 ATGGAAACGCGCGCTCAACAACAGTATGTTGCTCACTAGTCAAGGTCTCTACAGA 1176
 1021 ATGGAAATGACGCTCCACAACAGTATTTGCTCACTAGTCAAGGTCTGAGGTATAGA 1080
 1177 ACCTGTCTTCCACTTGTACAGAAAGCCCTCAATATGCTATCAACCAACGACATCT 1236
 1081 ACATTTATGCTCACTTATATAGAAAGCTTTATATATAGGATTAATTAATCAACATTA 1140
 1237 TCGCTTCTTACAGGAACAGATTCGCTATAGAACTCTTCTAATCTTCCATCGCTGT 1296
 1141 TCTGTTCTTACAGGACAGAAATTTGTTATAGAACTCTCTCAAAATTTGCCATCGCTGA 1280
 1297 TACAGAAAGCGGAACCGTTGATTCCTTGAAGAAATCCCAACAGAAACAAATGTG 1356
 1201 TACAGAAAGCGGAACGTTAGATTCGCTGATGAATTAACGCGCAAGAAATCAACGTTG 1260
 1357 CCACCGAGGAGGATTCCTCCACAGGTGAGCAGGTGCAATGTCGTTCCGATTC 1416
 1261 CCACCTTGGCAGGATTTAGTCAATGATTAAGGATTTCAATGATTTGCTTACGCTTT 1320
 1417 AGCAACAGTTCCGTCAGCATCATCAGAGCTCTATGTTCTCATGATTCATCTGATGCT 1476
 1321 AGTATATGATGATATATATATATATAGAGCTTCAACGTTTCTTGGCAGCATCGAGTCT 1380
 1477 GAGTTCAACATATCATTTCTTCTCTCAATCAACCAATCCATTTGACCAATCTACT 1536
 1381 GAATTTATATATATATATTTCTTCAATCAAAATTAACAAATCACTTTAAACAAATCTACT 1440
 1537 AACCTTGATCTGGAATCTTCTGTGTGAAAGGACAGGCTTCAAGAGGATGATTTCTT 1596
 1441 AATCTTGCTCTGGAATCTTCTGTGTGAAAGGACAGGATTTACAGAGGATGATTTCTT 1500
 1597 AGAAGAACTTCTCTGCGCAGATTTAGCAACCTCAGATTTAATCACTGACCACTTCT 1656
 1501 CGAAGAACTTCACTGCGCAGATTTCAACCTTAAAGAAATATATATCTGACCACTTATCA 1560
 1657 CAAGATATCTGTGAGGATTTGTTAGCATCTACCACTAATCTTGAATTCACACTCTCC 1716
 1561 CAAGATATCTGCGGTAACAAATTCGTCAGCTTCTACTCAAAATTTCAATTCATCAATCA 1620
 1717 ATGAGGAAGGCTATCAATCAGGATTAATCTTCCGCAACCATGTCAAGGCGGAGCAAC 1776
 1621 ATTAACGGAACCTATTAATCAGGATTAATTTTCAAGCACTATGATAGTGGAGATTAAT 1680
 1777 TTGCATTCGCGACCTTACAGAACCGTGGTTTCACTCTCTTCAACTTCTCTACGGA 1836
 1681 TTACAGTCCGGAACCTTAAAGACTGTAGGTTTACTCTCTCTTAACTTTTCAAAATGGA 1740
 1837 TCAAGCGTTTCAACCTTAAAGGCTCATGTGTTCAATTTCTGGCAATGAAGTATCATTTGAC 1896
 1741 TCAAGTATTTTAAAGTTAAAGTCAATGTCTTCAATTCAGGCAATGAAGTTATATAGAT 1800
 1897 CGTATGAGTTGTGCTGCGGAGGATTAACCTTCAGGCTGAGTA 1940

Db 1441 AATGTGCTCTGAACTTCTGTGTTAAAGACAGAGATTATACAGAGAGATATCTT 1500
Qy 1597 AGAAGACTTCTCTGCGCAGATTAGCACCTCAGAGATTACATCACTGACCACTTCT 1656
Db 1501 CGAAGAACTTACCTGCGCAGATTTCACACTTAAGAGTAATATTAATCTGACCACTTATCA 1560
Qy 1657 CAAAGATATCGTGTCAAGATTCTGTACGATCTACCACTTAATTCGAATTCACACCTCC 1716
Db 1661 CAAAGATATCGGTAAAGATTGCTACGCTCTACTACAAATTTACATTCATATCA 1620
Qy 1717 ATCAGCGAGAGCCTTATCAATCAGGTTACTTCTCCGACACATGTCAAGCGGACGAC 1776
Db 1621 ATTACCGAAGACCTATTAATCAGGTTAATTTTTCAGAACATATGAGTAGGAGTAAT 1680
Qy 1777 TTGCAATCCGCGACCTTACAGAACGTCGGTTTCACTACTCTTCAACTTCTTACAGGA 1836
Db 1681 TTACAGTCCGGAAGCTTTAGAGACTGTAGGTTTACTACTCCGTTTAACTTTTCAAAATGGA 1740
Qy 1837 TCAAGCGTTTTCACCTTACGCTCATGTGTTCATTTCTGCAATGAAGTGTACATTGAC 1896
Db 1741 TCAGGTGATTATGATTAGTTAGTGTCTCATGTCTTCAATTCAGGCAATGAAGTTATATGAT 1800
Qy 1897 CGTATGAGTTTGTGCTGCGGACGAGTTTACCTTCAGGCTGAGTA 1940
Db 1801 CGAATGAAATTTGTTCCGCGAAGTAACCTTTGAGGCAAAATA 1844

RESULT 14

US-10-102-469-1
; Sequence 1, Application US/10102469
; Publication No. US20030192078A1
; GENERAL INFORMATION:
; APPLICANT: Fischhoff, David A.
; APPLICANT: Fischhoff, Frederick J.
; TITLE OF INVENTION: SYNTHETIC PLANT GENES AND METHOD FOR PREPARATION
; FILE REFERENCE: 38-21 (13553) B
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: 08/434,105
; PRIOR FILING DATE: 1995-05-03
; PRIOR APPLICATION NUMBER: 07/959,506
; PRIOR FILING DATE: 1992-10-09
; PRIOR APPLICATION NUMBER: 07/476,661
; PRIOR FILING DATE: 1990-02-12
; PRIOR APPLICATION NUMBER: 07/315,355
; PRIOR FILING DATE: 1989-02-24
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1743
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE: OTHER INFORMATION: synthetic structural gene encoding B.t.k. HD-1 insecticidal prote
; OTHER INFORMATION: in
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1743)
; OTHER INFORMATION:
US-10-102-469-1

Query Match 42.4%; Score 1180.8; DB 12; Length 1743;
Best Local Similarity 80.0%; Pred. No. 0;
Matches 1389; Conservative 0; Mismatches 347; Indels 0; Gaps 0;

Qy 181 ATTGAACCGGTAACTTCCATGACATCTCTGCTTGTGACACAGTTTGTCTGACG 240
Db 7 ATAGAAATCGTTTACACCCCAATGATATTTCTTGTGCTTAAACCAATTTCTTTTGAAT 66
Qy 241 GAGTTCGTGCGAGGTGTGCTGCTTCTGAGCTAGTTGACATCATCTGGGATATCTTT 300
Db 67 GAATTTGTTCCGCGTGTGATTTTGTGTTAGACATGATTGATATATCTCGGGAAATTTT 126

Qy 301 GGTTCATCTCATGAGATGATCTCTGTGTCAAAATTGACAGTTTATCAACAGAGATC 360
Db 127 GGTTCCTCTCAATGGGACGCAATTTCTGTCAAAATTGAACAGCTCATCAACAGAGATC 186
Qy 361 GAAGATTTCCCGAAGAACCGGCAATCTCTAGSTTTGGAAGGATTTGACATCTCTACCA 420
Db 187 GAAGATTTCCGTAGGAATCAAGCAATTTCTAGATTTGAAGAGACTTAAGCAATCTTATCA 246
Qy 421 ATCTATGACAGAGCTTTCAGAGAGTGGGAAGCCGATCTTACTAACCCAGCTTCCGAG 480
Db 247 ATTTAGCAGAAATCTTTTGAAGAGTGGGAAGAGATCTTCTAATCCAGATTTAAGGA 306
Qy 481 GAAATGCTTATCAATTTCAACGATGAACAGGCTTGAACAAGCTATTCATTTGTC 540
Db 307 GAGATGCTTATCAATTTCAATGAACATGAACAGTGCCTTATCAACCGCTATTTCTTTT 366
Qy 541 GCAGTCCAGAACTTACCAAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 600
Db 367 GCAGTCCAGAAATTTATCAAGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 426
Qy 601 CTCAGCGTGTGAGAGCGTTAGCGTGTGTTGGCCAAAGTGGGATTCGATGTGCAACC 660
Db 427 CTCAGCTTTTGAAGAGTGTTCAGTGTTTGACAAAGTGGGATTTGATGCGCGACT 486
Qy 661 ATCAATGCGCTTACCAACGACTTACTAGCTGATTTGAAATCTACACGACACGCTGTT 720
Db 487 ATCAATGCTGTTATTAATGATTTTAACTAGGCTTATTTGGCAATATACGATCATGCTGTA 546
Qy 721 CGTTGTACCAACCTGCTTGGAGCGGTCTGGGGGTCTGATTTAGAGATTTGATTTAGA 780
Db 547 CGCTGTACAAATGCGGATTTAGCGGTGATTTGGGACCGGATTTCTACAGATTTGATCAG 606
Qy 781 TACAACAGTTTCAGAGAGATTTGACCCCTCAAGTTTGGACATTTGTCTCTCTCCG 840
Db 607 TACAACAGTTTCAGAGAGATTTGACCTTACATGATTTAATATGTTCTCTATTTCCG 666
Qy 841 AACTATGATTCAGAACTTACCTTATCGGTACAGTGTCCCACTTACAGAGAAATCTAT 900
Db 667 AACTATGATTTGTAAGATTTCAATTCGAATTCGAATTTCCCAATTTACAGAGAAATTTAT 726
Qy 901 ACTAATCCAGTTCTTGGAATCTTCAGAGTATGCTTCGTGTCTGTGCTGCAAGTATGGA 960
Db 727 ACAATCCAGTATTTAGAAATTTTGTATGATTTTGTGAGCTGCTGAGGCAATGAA 786
Qy 961 GGTCCATTCAGAGAGCCCACTTGTATGAGATCTTGAACAGATTAATCTATCTACCGAT 1020
Db 787 GGAATGATTTAGAGATTCACATTTGATGATATTTAATGATTAATACATCTATACGAT 846
Qy 1021 GCTCAGAGAGAGATTTAATCTGCTGTGACACCAATCATGCGCTTCTCAAGTTGATTC 1080
Db 847 GCTCATAGAGAGATTTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 906
Qy 1081 AGCGGCGCGAGTTTACTTCTCTCTATGGAATTTGGAAGAGCGCGCTCCACACAA 1140
Db 907 TCGGCGCGAGATTTCACTTCTGCTATATGGAATTTGGAAGAGAGCTCCACAA 966
Qy 1141 CGTATCGTGTCTCAATAGTCAAGTGTCTTACAGAACTTGTCTTCCACTTGTATACGA 1200
Db 967 CGTATGTGTCTCAATAGTCAAGTGTGTATGGAATTTATGATTTATGATTTATGAT 1026
Qy 1201 AGACCTTCAATATGCGGTATCAACACAGCAATTTCCGTTCTTGAACGAGAGCTTC 1260
Db 1027 AGACCTTCAATATGCGGTATCAACACAGCAATTTCTGTTGAGCGGAGCAATTT 1086
Qy 1261 GCTATGAGAACTTCTCAATTTGCTCATCGCTGTATACAGAAAAGCGAGATGAT 1320
Db 1087 GCTATGAGAACTTCTCAATTTGCTCATCGCTGTATACAGAAAAGCGAGATGAT 1146
Qy 1321 TCCTTGAAGCAATTTCCACACAGAACCAATGTGCGAGGCAAGATTTCTCCAC 1380
Db 1147 TCGCTGATGAAATTTACCGGACAGAAATTAACAACTGCGCACTTGAAGAGATTTATGAT 1206

QY 1381 AGTTGAGCCAGTGTCCATGTCCTCCGATTCAGCAACAGTCCGAGCATCATC 1440
 Db 1207 CGATTAGCCATGTTTCAATGTTTCGTTCAAGCTTTAGTAATAGTAGTAATATA 1266
 QY 1441 AGAGCTCTATGTTCTCATGATGATCTGTAGTGTGATGATCAATATATCCCTCC 1500
 Db 1267 AGAGCTCTATGTTCTCTGATGATCTGTAGTGTGATGATCAATATATCCCTCC 1326
 QY 1501 TCTCAATACCCCAATCCCATTTGACCAAGCTCTACTAATCTTGATCTGAACTTCTGTC 1560
 Db 1327 TCAAAATACCCCAATCCCATTTGACCAAGCTCTACTAATCTTGATCTGAACTTCTGTC 1386
 QY 1561 GTGAAGGACGAGGCTTCAAGAGGTGATTTCTTAGAAGAACTTCTCTGSCCAATT 1620
 Db 1387 GTTAAAGGACGAGGATTTACAGAGAGATATTTCTTGAAGAACTTCACTGSCCAATT 1446
 QY 1621 AGCAACCTCAAGATTAACATCACTGCAACCACTTTCTCAAAATATCGTGCAGATTCCT 1680
 Db 1447 TCAACCTTAAGATTAATATTAATGCAACCAATTAATCAAAAGATATCGGTAAAGATTCGC 1506
 QY 1681 TACGATCTACCACTTAATCTTGCAATTCACACCTTCATCGAGAGGCTATCATAG 1740
 Db 1507 TACGATCTACCACTTAATCTTGCAATTCACACCTTCATCGAGAGGCTATCATAG 1566
 QY 1741 GGTAACTTCTCCGAAACCATGTCAAGCGGAGCAACTTGAATCCGAGCTTCAAGAAC 1800
 Db 1567 GGAATTTTTCAGCAACTATGATGATGTGGAGTATTTACAGTCCGGAAGCTTTAGAGCT 1626
 QY 1801 GTGCTTCACTACTCTCTTCAACTCTCTCAACGATCAACGCTTTTCAACCTTACGCT 1860
 Db 1627 GTAGGTTTACTACTCCGTTTAACTTTCAATGATGATCAAGTGTATTTAAGTAAAGTCT 1686
 QY 1861 CATGCTTCAATCTTGCAATGAAGTATGACCTTATGATTTGTGCTGCTC 1916
 Db 1687 CATGCTTCAATCTTGCAATGAAGTATGACCTTATGATTTGTGCTGCTC 1742

RESULT 15

US-09-988-462-3

Sequence 3, Application US/09988462

Publication No. US20030046726A1

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

Desai, Nalini M.

Lewis, Kelly S.

Kramer, Vance C.

Warren, Gregory W.

Evola, Stephen V.

Crossland, Lyle D.

Wright, Martha S.

Merlin, Ellis J.

Lauis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/988,462

FILING DATE: 20-NO. US20030046726A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000
 APPLICATION NUMBER: US 08/459,504
 FILING DATE: 02-JUN-1995
 APPLICATION NUMBER: US 07/951,715
 FILING DATE: 25-SEP-1992
 APPLICATION NUMBER: US 07/772,027
 FILING DATE: 04-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 REFERENCE/DOCKET NUMBER: S-188051
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919)541-8587
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1947 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "Synthetic DNA"
 HYPOTHEICAL: NO
 FEATURE:
 NAME/KEY: misc.feature
 LOCATION: 1..1947
 OTHER INFORMATION: /product= "Truncated synthetic
 maize optimized cry1a(b) gene"
 /note= "Disclosed in Figures 1, 2, 3, 4 and 5 as basyn."
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-988-462-3
 Query Match 41.4%; Score 1153.8; DB 11; Length 1947;
 Best Local Similarity 76.6%; Pred. No. 0;
 Matches 1413; Conservative 0; Mismatches 432; Indels 0; Gaps 0;
 QY 97 ATGACAAACAACCCAAATCAACAAATGCAATTCATCAACATGCTGATGATCCAGAA 156
 Db 1 ATGACAAACAACCCAAATCAACAAATGCAATTCATCAACATGCTGATGATCCAGAA 60
 QY 157 GTTGAAGTCTGTGTGAGAGAAAGCATGAAACCGGTTTACATCTCCATGATCATCTCTTG 216
 Db 61 GTTGAAGTCTGTGTGAGAGAAAGCATGAAACCGGTTTACATCTCCATGATCATCTCTTG 120
 QY 217 TCTTGAACACAGTTTCTGCTCAGAGTTCGTGTCAGGTGCTGAGTTGTTCTGAGACTA 276
 Db 121 AGCTGACCAAGTTTCTGCTCAGAGTTCGTGTCAGGTGCTGAGTTGTTCTGAGACTA 180
 QY 277 GTTGAATCATCTGAGGATTTCTTTGTCATCTCAATGAGATGATGATCTCTGTCGAATT 336
 Db 181 GTTGAATCATCTGAGGATTTCTTTGTCATCTCAATGAGATGATGATCTCTGTCGAATT 240
 QY 337 GAGCAGTTGATCAACAGAGATGAAAGATGTCGCGAGAAACAGGACATCTTAGGTTG 396
 Db 241 GAGCAGTTGATCAACAGAGATGAAAGATGTCGCGAGAAACAGGACATCTTAGGTTG 300
 QY 397 GAAGATGACCAATCTCTACCAATCTATGACAGAGCTTACAGAGATGAGAAAGCCGAT 456
 Db 301 GAGGAGCTGACCAATCTCTACCAATCTATGACAGAGCTTACAGAGATGAGAAAGCCGAT 360
 QY 457 CCTACTAACCCAGCTCTCCGAGAGAAATGGTATTCATTCACAGATGATGACAGCCGC 516
 Db 361 CCTACTAACCCAGCTCTCCGAGAGAAATGGTATTCATTCACAGATGATGACAGCCGC 420
 QY 517 TTGACCAAGCTATCCATGTTGTCAGATCCAGAACTACCAAGTTCTCTTGGCTG 576
 Db 421 CTGACCAAGCTATCCATGTTGTCAGATCCAGAACTACCAAGTTCTCTTGGCTG 480
 QY 577 TACGTTCAAGAGCTAATCTTACCTCAGGTGCTTGAAGAGCTTGAAGCTGTTGGGCA 636
 Db 481 TACGTTCAAGAGCTAATCTTACCTCAGGTGCTTGAAGAGCTTGAAGCTGTTGGGCA 540
 QY 637 AGGTGGGATTCGATGCTGCAACCATCAATGAGCCGTTAACAAGACCTTACTAGCTGAT 696

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 21, 2003, 04:41:07 ; Search time 5203 Seconds
(without alignments)
13023.425 Million cell updates/sec

Title: US-09-980-650-6
Perfect score: 2788
Sequence: 1 aaataagatcttactgttc.....taccagagatcataatcag 2788

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hlc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hlc.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pin.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rtd.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	358.6	12.9	506	14	T24360
2	343.4	12.3	532	14	T15232
3	262	9.4	448	14	T14938
4	194	7.0	559	13	B082597

5	177.2	6.4	673	13	B0878720
6	171.8	6.2	255	13	BQ280286
7	167.8	6.0	686	13	B0893923
8	162	5.8	546	13	B0828900
9	161.6	5.8	551	13	B0828698
10	152.4	5.5	602	14	CA930016
11	151.6	5.4	600	13	B0826286
12	146	5.2	567	13	B0878721
13	140	5.0	659	14	CA929999
14	140	5.0	682	14	CA930552
15	133.6	4.8	588	14	B0827371
16	113.6	4.1	674	14	CA925612
17	107.6	3.9	314	14	CA929078
18	101.6	3.6	116	14	T14978
19	96.8	3.5	322	14	CA929990
20	94.4	3.4	576	14	CA929831
21	88.2	3.2	255	13	B0280285
22	87.4	3.1	414	13	B0893847
23	85.2	3.1	675	13	B0546804
24	83.2	3.0	603	12	BP120942
25	79.8	2.9	654	14	CD485177
26	75.8	2.7	628	14	CB329478
27	75.4	2.7	786	12	BP119110
28	73.4	2.6	819	12	BP119174
29	71.8	2.6	983	12	BG837559
30	71.2	2.6	312	12	BP119380
31	71	2.5	521	10	BG354049
32	70.6	2.5	179	14	CA929154
33	67.6	2.4	506	14	CA929067
34	65.6	2.4	494	9	AW746038
35	63.4	2.3	333	13	B0829081
36	63.4	2.3	383	10	BF586942
37	63.4	2.3	388	10	BF587479
38	61.4	2.2	629	12	BP118096
39	60.2	2.2	383	10	BF655880
40	59.6	2.1	554	12	BP118535
41	59.2	2.1	658	12	BP118003
42	59.2	2.1	662	12	BP118141
43	58.6	2.1	449	13	B0812453
44	58.2	2.1	630	12	BP117570
45	58.2	2.1	668	12	BP118481

ALIGNMENTS

RESULT 1
LOCUS T24360 506 bp mRNA linear EST 28-JUL-1995
DEFINITION csi1488 lambdaZAPST Ricinus communis cDNA clone pcrs1488, mRNA
Sequence.
ACCESSION T24360
VERSION T24360.1 GI:689178
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; euroside I; Malpighiales; Euphorbiaceae; Ricinus.
REFERENCE 1 (bases 1 to 506)
vanderloo, F.J., Turner, S. and Somerville, C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution
Tel: 4153251521
Email: crenandrew.stanford.edu
Seq primer: 73

FEATURES
source
Location/Qualifiers
1..506
/organism="Ricinus communis"
/mol_type="mRNA"

/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcrs148"
/clone.lib="lambdaZAPST"
/note="Vector: lambdaZAPII; Site 1: EcoRI; Site 2: XhoI; Poly(A)+ RNA was purified from developing stage III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of immature castor fruits. cDNA was synthesized and cloned into lambdaZAPII according to the instructions of the manufacturer (Stratagene); synthesis was primed from the poly(A) tail, and cloned directionally into XhoI (3') and EcoRI (5') sites. In few cases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate."

BASE COUNT 143 a 97 c 119 g 142 t 5 others

ORIGIN

Query Match 12.9%; Score 358.6; DB 14; Length 506;
Best Local Similarity 87.0%; Pred. No. 2.9e-97;
Matches 440; Conservative 0; Mismatches 53; Indels 13; Gaps 4;

OY 1959 GTTGTATGATCCCTGAGCCCATAGTGGTATCGTATCGAAATGGCTATGTTGAT 2018
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DB 1 GTTGTATGATCCCTGAGCCCATAGTGGTATCGTATCGAAATGGCTATGTTGAT 60
|||||

OY 2019 GTTAGGATGAGAGATTCCACACGGAACGCAATACAGTTGTGGCCATGCAAGCTTAT 2078
|||||
DB 61 GTTAGGATGAGAGATTCCACACGGAACGCAATACAGTTGTGGCCATGCAAGCTTAT 120
|||||

OY 2079 ACAGATGCAATCAGCTCTGCACTTTGAAAAGAGCAATCTATTGCTTAATGGAAG 2138
|||||
DB 121 ACAGATGCAATCAGCTCTGCACTTTGAAAAGAGCAATCTATTGCTTAATGGAAG 180
|||||

OY 2139 TGTTTAACTACTTACGGGTAGACGTCGGAGCTATGATGATATGATGCAATCT 2198
|||||
DB 181 TGTTTAACTACTTACGGGTAGACGTCGGAGCTATGATGATATGATGCAATCT 240
|||||

OY 2199 GCTGCAACTGATGCCACCCGCTGGCAAAATATGGATTAATGGAACCATGTAATCCAGA 2258
|||||
DB 241 GCTGCAACTGATGCCACCCGCTGGCAAAATATGGATTAATGGAACCATGTAATCCAGA 300
|||||

OY 2259 TCTAGTCTAGTTTATGACGACATCAGGAAACAGTGTGACAC- TTACGCTGCAAC 2317
|||||
DB 301 TCTAGTCTAGTTTATGACGACATCAGGAAACAGTGTGACAC- TTACGCTGCAAC 360
|||||

OY 2318 CAACATTTATGCGCGTTAGTCA-----AGGTTGGCTTCTACTATATA--TACACAC 2367
|||||
DB 361 CAACATTTATGCGCGTTAGTCA-----AGGTTGGCTTCTACTATATA--TACACAC 420
|||||

OY 2368 CTTTGTATCAAC--ATTGTTGGCTATATGCTCTGCTTGCAGCAAAATAGTGACA 2425
|||||
DB 421 TTTTGTATCAAC--ATTGTTGGCTATATGCTCTGCTTGCAGCAAAATAGTGACA 480
|||||

OY 2426 AGTATGATAGAGACTGTAGCAGTG 2451
|||||
DB 481 AAGTTGGTATGAGGCTGTAGAGTG 506
|||||

RESULT 2

LOCUS T15232 532 bp mRNA linear EST 28-JUL-1995
DEFINITION c18826 lambdaZAPST Ricinus communis cDNA clone pcrs826 similar to agglutinin B chain, mRNA sequence.
ACCESSION T15232
VERSION T15232.1 GI:688885
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; euroside 1; Malpighiales; Euphorbiaceae; Ricinus.
REFERENCE 1 (bases 1 to 532)
AUTHORS vandelaar,F.J., Turner,S. and Somerville,C.

TITLE
JOURNAL
COMMENT
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St., Stanford, CA 94305
Tel: 4153251521
Email: crs@andrew.stanford.edu
Seq primer: T3.
Location/Qualifiers

FEATURES
source
1..532
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone.lib="lambdaZAPST"
/clone="pcrs826"
/note="Vector: lambdaZAPII; Site 1: EcoRI; Site 2: XhoI; Poly(A)+ RNA was purified from developing stage III to stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760, 1982) endosperm plus embryo of immature castor fruits. cDNA was synthesized and cloned into lambdaZAPII according to the instructions of the manufacturer (Stratagene); synthesis was primed from the poly(A) tail, and cloned directionally into XhoI (3') and EcoRI (5') sites. In few cases, sequence data indicated that this directionality was reversed. Partial cDNA clones predominate."

BASE COUNT 140 a 111 c 121 g 143 t 17 others

ORIGIN

Query Match 12.3%; Score 343.4; DB 14; Length 532;
Best Local Similarity 81.8%; Pred. No. 1.3e-92;
Matches 435; Conservative 0; Mismatches 88; Indels 9; Gaps 4;

OY 2193 AATACGCTGCACTGATGCAACCCGCTGGCAAAATATGGATTAATGGAACCATGTAAT 2252
|||||
DB 1 AATACGCTGCACTGATGCAACCCGCTGGCAAAATATGGATTAATGGAACCATGTAAT 60
|||||

OY 2253 CCCAGATCTAGTCTAGTTTATGACGACATCAGGAAACAGTGTGACACCTTACGCTG 2312
|||||
DB 61 CCCAGATCTAGTCTAGTTTATGACGACATCAGGAAACAGTGTGACACCTTACGCTG 120
|||||

OY 2313 CAACCAACATTTATGCGCTTATGACGACGTTGGCTTCTTATATATCAACCTTTT 2372
|||||
DB 121 CAACCAACATTTATGCGCTTATGACGACGTTGGCTTCTTATATATCAACCTTTT 180
|||||

OY 2373 GTTCAACCAATTTGCGCTTATGATGCTGCTGCTTGCAGCAAAATAGTGACAAGTATG 2432
|||||
DB 181 GTTCAACCAATTTGCGCTTATGATGCTGCTGCTTGCAGCAAAATAGTGACAAGTATG 240
|||||

OY 2433 ATAGAGACCTGACAGTGAAGGCTGAACACAGTGGCTCTTTATGACAGTGTCA 2492
|||||
DB 241 TTAGAGACCTGACAGTGAAGGCTGAACACAGTGGCTCTTTATGACAGTGTCA 300
|||||

OY 2493 ATAGCTCTGCAAAAACGAGATTA--TTGCCCTTACAAGTAT--TCTATATACGGG 2547
|||||
DB 301 ATAGCTCTGCAAAAACGAGATTA--TTGCCCTTACAAGTAT--TCTATATACGGG 360
|||||

OY 2548 AAACAGTTGTAAGATCCTCTCTT--GTGGCCCTGACATCTCTGACCAACAGTGAATTT 2605
|||||
DB 361 AAACAGTTGTAAGATCCTCTCTT--GTGGCCCTGACATCTCTGACCAACAGTGAATTT 420
|||||

OY 2606 C--AAGAATGATGAACCATTTTAATTTGTATAGTGATTTGTATAGATGAGGCGA 2663
|||||
DB 421 C--AAGAATGATGAACCATTTTAATTTGTATAGTGATTTGTATAGATGAGGCGG 480
|||||

OY 2664 TCGATCCGAGCCTTAACCAATCATCTTACCTCTCCATGAGGCCCA 2715
|||||
DB 481 TCGATCCGAGCCTTAACCAATCATCTTACCTCTCCATGAGGCCCA 532
|||||

RESULT 3

LOCUS T14938 448 bp mRNA linear EST 28-JUL-1995

DEFINITION crs424 lambdaZAPST Ricinus communis cDNA clone pcrs424 similar to
ricin D chain B, mRNA sequence.
ACCESSION T14938
VERSION T14938.1 GI:688594
KEYWORDS EST.
SOURCE Ricinus communis (castor bean)
ORGANISM Ricinus communis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
REFERENCE
1 (bases 1 to 448)
vanderloo, F.J., Turner, S. and Somerville, C.
Expressed sequence tags from developing castor seeds
Plant Physiol. 108, 1141-1150 (1995)
JOURNAL Contact: Somerville CR
Carnegie Institution
Carnegie Institution, 290 Panama St, Stanford, CA 94305
Tel: 4153251521
Email: crs@andrew.stanford.edu
Seq primer: T3.
Location/Qualifiers
1..448
/organism="Ricinus communis"
/mol_type="mRNA"
/strain="Baker 296"
/db_xref="taxon:3988"
/clone="pcrs424"
/note="Vector: lambdaZAPST; Site 1: EcoRI; Site 2: XhoI;
Poly(A)+ RNA was purified from developing stage III to
stage V (Greenwood & Bewley, Can. J. Bot. 60:1751-1760,
1982) endosperm plus embryo of immature castor fruits.
cDNA was synthesized and cloned into lambdaZAPII according
to the instructions of the manufacturer (Stratagene);
synthesis was primed from the poly(A) tail, and cloned
directionally into XhoI (3') and EcoRI (5') sites. In few
cases, sequence data indicated that this directionality
was reversed. Partial cDNA clones predominate."
BASE COUNT 118 a 81 c 92 g 140 t 17 others
ORIGIN
Query Match 9.4%; Score 262; DB 14; Length 448;
Best Local Similarity 96.4%; Pred. No. 7.3e-68;
Matches 268; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 2488 GTTCAATACGTCCTCAGCAAAACGAGATAATGCTTACCAAGTATCTAATATACGG 2547
1 GTTCAATACGTCCTCAGCAAAACGAGATAATGCTTACCAAGTATCTAATATACGG 60
DB 2548 AACAGTTGTAAGATCCTCTCTTGCGCCCTGCATCCTCTGCGCAACGATGATGTTCA 2607
61 AACAGTTGTAAGATCCTCTCTTGCGCCCTGCATCCTCTGCGCAACGATGATGTTCA 120
QY 2608 AGATGATGAAACCAATTTTAAATTTGTAAGTGAATGCTTGAATGAGCGCATCGG 2667
121 AGATGATGAAACCAATTTTAAATTTGTAAGTGAATGCTTGAATGAGCGCATCGG 180
DB 2668 ATCCGAGCCTTAAACAAATCAATCTTTACCCCTCAGTGAACCCAAACCAATATGAT 2727
181 ATCCGAGCCTTAAACAAATCAATCTTTACCCCTCAGTGAACCCAAACCAATATGAT 240
QY 2728 TACCATTTATTTGATGACAGATTACAAGCTTGTGAG 2765
241 TACCATTTATTTGATGACAGATTACTCTCTGACAGTG 278
RESULT 4
LOCUS BU825997 559 bp mRNA linear EST 15-OCT-2002
DEFINITION UK115TE03 Populus apical shoot cDNA library Populus tremula x
Populus tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION BU825997
VERSION BU825997.1 GI:23998128

KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Malpighiales; Salicaceae; Populus.
REFERENCE
1 (bases 1 to 559)
Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
Unpublished
JOURNAL Contact: BHALERAO RUPALI R.
Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
Location/Qualifiers
1..559
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="apical shoot"
/clone_id="Populus apical shoot cDNA library"
BASE COUNT 168 a 123 c 122 g 146 t
ORIGIN
Query Match 7.0%; Score 194; DB 13; Length 559;
Best Local Similarity 59.4%; Pred. No. 4.3e-47;
Matches 329; Conservative 0; Mismatches 225; Indels 0; Gaps 0;
QY 1933 GCTGAGTACTGAGAATTCATGCTGATGTTGTATGATCTGACCCCATGCTGCTATCG 1992
6 GCCCTGTCGCGCAAGAAATGACATGTTGTTCTGTTCAAACTCCACACACATGTTG 65
DB 1993 TAGTGCATATGCTCTATGTTGTTATGTTAGGATGGAAGTTCACACAGGAACGCA 2052
66 TTGGCATTAATTAATTTGCGTTGACGTGTTCTTGAACTCTACTTTGATGGAACCTTAG 125
QY 2053 TACAGTTGCGCCATGCAAGTCTAATACAGATGCAATACAGCTGCGACTTTGAAAGAG 2112
126 TACAGTTGCGCCATGCAAGTCTAATACAGATGCAATACAGCTGCGACTTTGAAAGAG 185
QY 2113 ACAATACTATTCATCTAATGGAAGTGTTTAATCTAATGCGGTACAGTCCGGAGTCT 2172
186 ACGGAACATTCATCTAATGGAAGTGTTTGCGCACAAACGGCAAGTCCAGGAAGCT 245
QY 2173 ATGTGATGATTTATGATTTCAATCTGCTGCAACTGATGCCACCCGCTGCAATATGGG 2232
246 ATGTGATGATTTATGATTTCAATCTGCTGCAACTGATGCCACCAATTTGGAAATACAA 305
DB 2223 ATATGGAACCATATAATATCCGATCTAGTCTAGTTTGGACGCGCATCAGGAACA 2292
306 AGATGCGCTCATCTAATACCCCTCTGCTGCTAGTTTGAACCTCAAAAGTCAGGAAAA 365
QY 2293 GTGTACACACTTACCGTGCAACCAATTTATGCGTTAGTCAAGTTGGCTTCTTA 2352
366 GTGTACCGCTCATCTAATACCCCTCTGCTGCTAGTTTGAACCTCAAAAGTCAGGAAAA 425
DB 2353 CTAAATATACCAACCTTTTGTACACCAATTTGTTGGCTATATGTTGCTGCTTGAAG 2412
426 CCGATGTTTCAAAACCAACCAAGTCAATGTCGCGCTTTGGAGTCACTGCTTGAAT 485
QY 2413 CAATATGAGACAAGTATGATGATGAGACTGACAGTGAAGAAAGCTGAACAACAGTGGG 2472
486 TTAAACAATATGTCCTCAAAAGTTACCAAGTGCCTGAGAGAACAAAGTGAACAATTTGA 545
DB 2473 CTCTTTATGACAT 2486
QY 546 ATTTTACGACAT 559

[illegible]

Db	664	TTAACA	669	
RESULT 6				
LOCUS	B0280286		255 bp	mRNA linear EST 01-MAY-2003
DEFINITION	PAC0000000001474	Pioneer AF-1 array	Zea mays cDNA	mRNA sequence.
ACCESSION	BQ280286			
VERSION	BQ280286.1	GI:30270760		
KEYWORDS	EST.			
SOURCE	Zea mays			
ORGANISM	Zea mays			
REFERENCE	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.			
AUTHORS	1 (bases 1 to 255)			
TITLE	Habben J.			
JOURNAL	Analysis of gene expression in drought stressed maize			
COMMENT	Unpublished			
FEATURES	Contact: Habben J			
source	Trait and Technology Development, Agronomic Traits			
	Pioneer Hi-Bred International, Inc.			
	7250 N 62nd Ave., P.O. Box 552, Johnston, IA 50131-0552, USA			
	Tel: 515 270 4130			
	Fax: 515 334 4778			
	Email: jeffrey.habben@pioneer.com.			
BASE COUNT	47 a	93 c	65 g	50 t
ORIGIN				
Query Match	6.2%	Score 171.8;	DB 13;	Length 255;
Best Local Similarity	79.6%	Pred. No. 1.6e-40;		
Matches 203;	Conservative	0;	Mismatches 52;	Indels 0;
			Gaps 0;	
QY	157	GTGAAGTACTTGTGTGAGAA	CGGATTGAA	CCGGTTACATCTCCATCGACATCTCCTTG 216
Db	61	GTGAGGGTGTCTGGCGGGAGCGGATCGAGAC	CCGGTTACACCCGATCGACATCTCCTTC 120	
QY	217	TCCTTGACACAGTTTCTGCTAGCGAGTTCGTGCGAGTGTGCGAGTTCGTCTCTCGACTA	276	
Db	121	TCCCTTACACCCAGTTCTCTCTCTCCGAGTTCGTGCGAGCGCGGCTTCGTGCTCGGCTTC	180	
QY	277	GTTGACATCATCTGSGGGATCTTGTGTCATCTCAATGAGATGATTCCTGTGCAAAATT	336	
Db	181	GTGACATCATCTGGGGCATCTTGGCGCCGTCCTCCAGTGGACGCGCTTCTGTGCAATC	240	
QY	337	GAGCAGTTGATCAAC	351	
Db	241	GAGCAGTTAATTAAAC	255	
RESULT 7				
LOCUS	B0893923		686 bp	mRNA linear EST 17-OCT-2002
DEFINITION	P084806	Populus petiolaris cDNA library	Populus tremula cDNA	5 prime,
ACCESSION	B0893923			
VERSION	B0893923.1	GI:24104988		
KEYWORDS	EST.			
SOURCE	Populus tremula			
ORGANISM	Eukaryote: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; rosids			

REFERENCE	1 (bases 1 to 686)	euroids 1; Malpighiales; Salicaceae; Populus.
AUTHORS	Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.	
TITLE	The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries	
JOURNAL	Unpublished	
COMMENT	Contact: BHALERAO RUPALI R. Umea Plant Science Center Department of Plant Physiology University of Umea, 901 87 Umea, Sweden Tel: +46 90 786 5279 Fax: +46 90 786 6676 Email: rupali.bhalerao@planphys.umu.se.	
FEATURES	location/Qualifiers	
source	1..686	
	/organism="Populus tremula"	
	/mol_type="mRNA"	
	/db_xref="taxon:113616"	
	/issue_type="petioles"	
	/clone_lib="Populus petioles cdna library"	
BASE COUNT	197 a 149 c 161 g 178 t	1 others
ORIGIN		
Query Match	6.0%; Score 167.8; DB 13; Length 686;	
Best Local Similarity	60.8%; Pred. No. 4,7e-39;	
Matches 291; Conservative	0; Mismatches 187; Indels 1; Gaps 1;	
Oy	1933 GCTGAGTACTGAGAAATTCATCTGATGTTTGTATGATGCTGAGCCCTAGTGGCTATG	1992
Db	209 GCTCTGTCGTCGCAAAAATAATACATGTTGTTCTGCTGCAAAAGTCCACACACATG	268
Oy	1993 TAGGTGCAATGTCCTATGTTGTTAGATGTTAGGATGAAAGATTCCACACGAAACGCA	2052
Db	269 TTGGCATTAATAATTTGTCGCTTGACGCTGTTCTTGAACCTGACTAGATGAAACGTA	328
Oy	2053 TACAGTGTGGCCATGCAAGTCTAATACAGATGCAATGACCTGCACTTTGAAAGAG	2112
Db	329 TACAGTGTACCCGCTGAATCTAACGGAATGGAATCAACAAATGAGCTTGAGAGAA	388
Oy	2113 ACAATACTATTGATCTAATGGAAGTGTTTAACTACTTACGGGTACAGTCCGGAGTCT	2172
Db	389 ACGGAACATTCAATCTTAAGAAAGTGTTTGGCAACAAACGGCAAGTCCAGGAAGCT	448
Oy	2173 ATGTGATGATCTAATGATTGCAATACGTCTGCAACTGATGCCACCCGCTGGCAATATGG	2232
Db	449 ATGATATTATCTCGACGCAACAGGTAAGGCTAGAGCCACAAATTTGAAAGTACAA	508
Oy	2233 ATAAATGGAACCATATAAATCCAGATCTAGTCTAGTTTATGACGACATCAGGAA	2292
Db	509 AGATAGGCTCATCTTAACCCCTCCTGCTGCTAGTATTGACCTCAAAAGTCGGGAAA	568
Oy	2293 GTGTACCACTTAAGGTGCAAAACCAACATTTATGCGCTTAATGTCAGATTGGCTCTTA	2352
Db	569 GTGGTCTCCTACTAC-C-TGGGAACCAATGTTTATGCTTGGGCGCAAGTTGGAATTTCA	627
Oy	2353 CTAATTAATACCAACCTTTGTTCAACCATTTGGGCTATATATGATGTCGCTTGCA	2411
Db	628 CCAAGTCTTCAAAACCATCACCGAAGTCCATTTCGGGCTTTGGGACTACTGCTTGGA	686
RESULT 8		
LOCUS	BUS28900	546 bp mRNA linear EST 15-OCT-2002
DEFINITION	K030P6P Populus apical shoot. cdna library Populus tremula x	
ACCESSION	BUS28900	
VERSION	BUS28900.1	GI:24004289
KEYWORDS	EST.	
SOURCE	Populus tremula x Populus tremuloides	
ORGANISM	Populus tremula x Populus tremuloides	
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; rosids; euroids 1; Malpighiales; Salicaceae; Populus.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 546)	Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.	The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries	Unpublished	
	Contact: BHALERAO RUPALI R.			
	Umea Plant Science Center			
	Department of Plant Physiology			
	University of Umea, 901 87 Umea, Sweden			
	Tel: +46 90 786 5279			
	Fax: +46 90 786 6676			
	Email: rupali.bhalerao@plantphys.umu.se.			
	Location/Qualifiers			
	1. 546			
	/organism="Populus tremula x Populus tremuloides"			
	/mol_type="mRNA"			
	/db_xref="taxon:47664"			
	/cbase_type="apical shoot"			
	/clone_id="Populus apical shoot cDNA library"			
BASE COUNT	154 a	124 c	125 g	143 t
ORIGIN				
Query Match	5.8%	Score 162;	DB 13;	Length 546;
Best Local Similarity	58.24;	Pred. No. 2.4e-37;		
Matches 313;	Conservative	0;	Mismatches 210;	Indels 15;
			Gaps	1;
QY	2155	GGTACAGTCCGGAGTCTATGTGTATGATCTATGATTTGCAATACCTGCTGCAACTGATGCCA	2214	
Db	6	GGCACAAGTACGAGAAAGTATGATTTATCTCTGACTGCACCAAGGTGAAGGCTAGCCCA	65	
QY	2215	CCCCGTGGCAATATGGAATATGGAACCATCATTAATCCCAAGTCTAATGCTATGTTTGA	2274	
Db	66	CAATTTGGAAAGTACAAAGAGATGGCTCCATCTCCACACCCCTCTCATGATTTTGA	125	
QY	2275	CAGCGACATCAGGAAACAGTGTACCACTTACGCTGCAAAACCAATTTATGCCGTTA	2334	
Db	126	CTTAAAGTCGGGAAAGTGTGCTCTCTACCTGCTGGAACCAAGTTATGCTTGG	185	
QY	2335	GTCAAGTTGGCTTCTACTAATATATACAACTTTTGTTCACCAAGTGTGGGCTAT	2394	
Db	186	GCCAAAGTTGAAATTTTACACAGTGTTCACAAACCATCACGAACTCATGTGCGGGCTTT	245	
QY	2395	ATGCTGTGCTTCCAGCAAAATGATGGAACAAGTATGATGATGAGAGCTGTAGCAGTGA	2454	
Db	246	GGGACTACTGCTTGAATTTTACAAAAGGCTCCAAAGTTTACCAAGTGTGTAAGAACA	305	
QY	2455	AGGCTGAACAACAGTGGGCTTTTATGACATGATGTTCAATAGTCTCAGCAAAACCGAG	2514	
Db	306	AGACTGAACAAAATGGAATCTTTACGCCCGATGTTGCATGAGGTTGATGCAACACAG	365	
QY	2515	ATAATGCTTACAGATGATCTTAATATACGGGAAACAGTTGTTAAGTCTCTCTGTG	2574	
Db	366	ATTGTGCTTACTACGATGGAATATCCAAAGAAAGTCTGCTGTGTCTCTGTGA	425	
QY	2575	GCCCTGATCCTCTGCGCAACGATGATGTT-----CAAGATGAGAA	2619	
Db	426	GCCCTGTGATCTTAACCAAGTTGGAAGTTGGGACAGCCAGCGCAAAAGCTATTTCC	485	
QY	2620	CCATTTTAATTTGATATGATGATTTGTTGATGATGAGGCGATCGATCCGAGCTT	2677	
Db	486	CCATTTTGAAACGTGAATATAGCTTTGTGTGATGTGAAGCTATTCATTTAAACTT	543	
RESULT 9				
BUS28698	BUS28698	551 bp	mRNA	linear
LOCUS	BUS28698	551 bp	mRNA	linear
DEFINITION	K02695P Populus apical shoot cDNA library Populus tremula x			
ACCESSION	BUS28698			
VERSION	BUS28698.1	GI:24003857		
SOURCE	Populus tremula x Populus tremuloides			
ORGANISM	Populus tremula x Populus tremuloides			

REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
TITLE	1 (bases 1 to 551)
JOURNAL	Umeberg, P., Bhalerao, R.R., Jansson, S. and Sterky, F.
COMMENT	The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
FEATURES	Unpublished
source	Contact: BHALERAO RUPALI R. Umea Plant Science Center Department of Plant Physiology University of Umea, 901 87 Umea, Sweden Tel.: +46 90 786 5279 Fax: +46 90 786 6676 Email: rupali.bhalerao@plantphys.umu.se. Location/Qualifiers
BASE COUNT	156 a 118 c 126 g 151 t
ORIGIN	1..551
	/organism="Populus tremula x Populus tremuloides"
	/mol_type="mRNA"
	/db_xref="taxon:47664"
	/tissue_type="apical shoot"
	/clone_lib="Populus apical shoot cDNA library"
Query Match	5.8%; Score 161.6; DB 13; Length 551;
Best Local Similarity	57.9%; Pred. No. 3.2e-37;
Matches 315, Conservative 0, Mismatches 214; Indels 15; Gaps 1;	
OY	2166 GGAGCTCATGATGATCTATGATTGGCAATTCGTGCGACACTGATGCACCAGCCGTGGCAA 2225
Dd	2 GGAAGCTTATGTAATGATCTCTGACTGCACAAGAAGTTAAAGCTTAGCGCCACATTTGGAAA 61
OY	2226 ATATGGATAATGGAACCATCATTAATCCAGATCTACTCTAATTTTTAGCAGCACATCA 2285
Dd	62 GTACAAAAAGATGGTGCTCATCTACACCCCTCGTGCATGATTATGACCTCAAAAGTCG 121
OY	2286 GGGAACAGTGTGATCCACACTTACGGTGCAAACCAATTTATGCCGTTAGTCAAAGTTGG 2345
Dd	122 GGGAAAGATGCTCCCTACCTACACCTTGGAAACCAATGTTTATGCTTGGGCCAAAGTTGG 181
OY	2346 CTCTCTACTAATTAATACACACTTTTGTTCACACATTTGTGGGCTATATGTCGTGCG 2405
Dd	182 AATTTACCAAGTGTTCACAAACCATACCGAAGTTCATTTGCGGCTTTGGGACTACTGCG 241
OY	2406 TTGCAGCAAAATAGTGAACAATATGATAGTAGNAGACTGTAGACAGTGAAGAAAGCTGAC 2465
Dd	242 TTGGAATTTTAAACAAAAGAGTCCCAAGATTTAGGCTACTGATGATGATGAACAACAGCTGAC 301
OY	2466 CAGTGGGCTCTTTATGACAGATGTTCAATACGTCCTCAGCAAAACCGAGATTAATTCCTT 2525
Dd	302 AAATGGAATCTTTTACGCCGATGTTGCATTAAGGGTTGATGCAAAACACAGATTTTGGCTTC 361
OY	2526 ACAAGTATTTCTAATATACGGGAAACAATTGTAAGATCCCTCTCTTTGGGCCCTGACACC 2585
Dd	362 ACTACCGATGAGAAATACAAAGGAAGCTCGGTCCTGTTGTCCTTTGAGCCCTGTGTGCA 421
OY	2586 TCTGGCCACAGATGATGTT-----CAAGAATGATGAGAACATTTTAAT 2630
Dd	422 TCTAACCAACGTTGGAAGTTTGGGACAGCCACGGCAAAAGCTTATTTCCCATTTTGAAC 481
OY	2631 TTGTAATAGTATTTGGTGTATAGATGTGAGGCGATGGAATCCGAGCCTTAAACAAATCAT 2690
Dd	482 GTGAATATATGCTTTGGTGTGATGATGATGATGATTCATTTCAATTAACCTTGTCAAAATAT 541
OY	2691 CTTT 2694
Dd	542 TAAT 545

DEFINITION	mtu2ca.pe.a07 Aspen apex cDNA Library Populus tremuloides cDNA.					
ACCESSION	CA930016					
VERSION	CA930016.1 GI:27418497					
KEYWORDS	EST.					
SOURCE	Populus tremuloides (quaking aspen)					
ORGANISM	Populus tremuloides					
REFERENCE	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; rosids ; eurosids I; Malpighiales; Salicaceae; Populus.					
AUTHORS	Ranjana,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai ,C-J.					
TITLE	Expressed sequence tags from Aspen					
JOURNAL	Unpublished					
COMMENT	Contact: Tsai C-J Plant Biotech Research Center Michigan Technological University, School of Forest Resources & Environmental Science 1400 Townsend Drive, Houghton, MI 49931-1295, USA Tel: 906 487 2914 Fax: 906 487 2915 Email: chtsai@mtu.edu. location/Qualifiers					
FEATURES	1..602					
source	/organism="Populus tremuloides" /mol_type="mRNA" /db_xref="taxon:3693" /clone_lib="Aspen apex cDNA library" /note="Organ: apex"					
BASE COUNT	171 a	132 c	137 g	161 t	1 others	
ORIGIN						
Query Match	5.5%; Score 152.4; DB 14; Length 602;					
Best Local Similarity	58.3%; Pred. No. 2.1e-34;					
Matches	295;	Conservative	0;	Mismatches	196;	Indels 15; Gaps 1;
OY	2236	ATGGAACCATATTAATCCAGATCTAGTCTTAGTTTAGCAGCACATCAGGGAAACTGT	2235			
DB	7	ATGGCTCCATCTTAAACCCCTCCCGTCACATGATTTGACCTCAAAGTCGGGAAAAAGTG	66			
OY	2296	GTAACACACTTACGGGTGCAACAACAATTTATGCGTTAGCAAGTTTGCTCTACTA	2355			
DB	67	GCTCCCTCCTACCTTGGAACCAATGTTTATGCTTGCGCCAAAGCTTGGAATTCACCA	126			
OY	2356	ATAATACACAACCTTTTGTATACAACAATGTTGGGCTATATGTCGTGCTTGCAAGCAA	2415			
DB	127	GTGTTTAAAACATACACCAGAAGTCATATGTCGGGCTTTGGGACATAGCTTGGAAATTTA	186			
OY	2416	ATAGTGACAAATATGATAGAGACTGTAGCACTGTAAGGCTGGAACACACAGTGGGCTC	2475			
DB	187	ACAAAAGGTGCCAAAGTTTACCCAAGTCGTAAGAAACMAACATGAAACMAAAATGGAATT	246			
OY	2476	TTTATGCAGATGTTTCATATAGTCTCCTCAGCAAAACCGAGATATTTGCTTACAGATGT	2535			
DB	247	TTTACGCAATGTTTCATATAGGTTGTCGAAACACAGATTTGTGCTTAACTAGCAGATG	306			
OY	2536	CTAATATACGGGAAACAGTTGTTAAGATCCTCTCTTGTCGCTTGCAATCTCTG6CCAAC	2595			
DB	307	GAAATACCAAGGAAGCTTGTCGTGTCGTGTCCTTTGTAAGCCGTGTGATCTTAACCAAC	366			
OY	2596	GATGATGTT-----CAAGAAATGATGAACCATTTTAAATTTGATATAGTG	2640			
DB	367	GTGGACCTTTGGGGACAGCCACGGCAAGCTTATTTTCCCATTTTGAAACGTGAATATAG	426			
OY	2641	GATTGATGTTAGATGTGAGGAGATCCGATCCGAGCTTAAACATATCTTTTAAACCTC	2700			
DB	427	CTTTGATGTTGATGATGAGCTATTCATCTTCAAACCTGTCTCAAATAATTTATTGGGATT	486			
OY	2701	TTCATGTGATGCCAAACCAATATAGG	2726			
DB	487	TCAACGAGAGAGCTAACCAAGTATAGG	512			

RESULT 11
 LOCUS BU826286 600 bp mRNA linear EST 15-OCT-2002
 DEFINITION UN18G11 Populus apical shoot cDNA library Populus tremula x
 Populus tremuloides cDNA 5 prime, mRNA sequence.
 ACCESSION BU826286
 VERSION BU826286
 KEYWORDS GI:23998729
 SOURCE
 ORGANISM
 Populus tremula x Populus tremuloides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; Populus.
 1 (bases 1 to 600)
 UNEBERG, P., BHALERAO, R.R., JANSSON, S. and STERKY, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 Unpublished
 Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 Location/Qualifiers
 1..600
 /organism="Populus tremula x Populus tremuloides"
 /mol_type="mRNA"
 /db_xref="taxon:47664"
 /issue_type="apical shoot"
 /clone_lib="Populus apical shoot cDNA library"
 BASE COUNT 181 a 125 c 132 g 158 t
 ORIGIN
 Query Match 5.4%; Score 151.6; DB 13; Length 600;
 Best Local Similarity 61.3%; Pred. No. 3.7e-34;
 Matches 244; Conservative 0; Mismatches 154; Indels 0; Gaps 0;
 Oy 1933 GCTGAGTCTGAGAAATTCATGCTGATGTTTGTATGATGATCCGAGCCCTAGTGCCTATCG 1992
 Db 203 GCCCTGTCGCCAAGAAATACGATGTTGTTCTGTTCAAGTCCACACAACACATTTG 262
 Oy 1993 TAGGTGCAATGCTCTATGCTGTTGATGTTAGGATGAGAATTCACAACGAAACGCA 2052
 Db 263 TTGGCATTAATTAATTTGTCGCTGACGCTGTTCTTGAATCTACTTTGATGAAATCTAG 322
 Oy 2053 TACAGTTGGCCATGCAAGTCTTAATACAGATGCAATCACTGACTTGAAGTGAAGAG 2112
 Db 323 TACAGTTGATCCCGTGAATCTTAACGAGATGTAATCAACATGAGAGCTTGGAGAAGA 382
 Oy 2113 ACAATACTATTCGATCTAATGGAAGTGTAACTCACTTACGGGATACGTCGGAGTCT 2172
 Db 383 ACGGAACCATTCATTAAGGCAAGTGTGGCCACAACGCAACAGTCCAGGAAGCT 442
 Oy 2173 ATGTGATGATCTATGATGCAATACTGCTGCAACTGATGACACCCGCTGCGCAATATG 2232
 Db 443 ATGTATTTATCTCTGATCGCAACAGTGAAGGCTTAAGGCCACATTTGGAATAACAA 502
 Oy 2233 ATTAATGAACCATCTAATAATCCAGATCTAGTCTAGTTTACGACGCACTAGGAAACA 2292
 Db 503 AGGATGGCTCATCTTAACCCCTCTGCTCACTGATTGACCTCAAGTCAAGGAGGAAA 562
 Oy 2293 GTGGTACCACTTACGGTGAACCAACATTTAGGCC 2330
 Db 563 GTGGCTCCCTACTCACTTGAACCAATGTTATGCC 600

RESULT 12
 LOCUS BU878721 567 bp mRNA linear EST 16-OCT-2002
 DEFINITION V050F07 Populus flower cDNA library Populus balsamifera subsp.
 trichocarpa cDNA 5 prime, mRNA sequence.
 ACCESSION BU878721
 VERSION BU878721
 KEYWORDS GI:24070245
 SOURCE
 ORGANISM
 Populus balsamifera subsp. trichocarpa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; eurosids I; Malpighiales; Salicaceae; Populus.
 1 (bases 1 to 567)
 UNEBERG, P., BHALERAO, R.R., JANSSON, S. and STERKY, F.
 The poplar tree transcriptome: Analysis of expressed sequence tags
 from multiple libraries
 Unpublished
 Contact: BHALERAO RUPALI R.
 Umea Plant Science Center
 Department of Plant Physiology
 University of Umea, 901 87 Umea, Sweden
 Tel: +46 90 786 5279
 Fax: +46 90 786 6676
 Email: rupali.bhalerao@plantphys.umu.se.
 Location/Qualifiers
 1..567
 /organism="Populus balsamifera subsp. trichocarpa"
 /mol_type="mRNA"
 /sub_species="trichocarpa"
 /db_xref="taxon:3694"
 /clone_lib="Populus flower cDNA library"
 /note="Organ: flower"
 BASE COUNT 174 a 119 c 129 g 145 t
 ORIGIN
 Query Match 5.2%; Score 146; DB 13; Length 567;
 Best Local Similarity 60.7%; Pred. No. 1.8e-32;
 Matches 239; Conservative 0; Mismatches 155; Indels 0; Gaps 0;
 Oy 1933 GCTGAGTCTGAGAAATTCATGCTGATGTTTGTATGATGATCTGAGCCCTAGTGCCTATCG 1992
 Db 174 GCTCTGTCGTCGCCAAGAAATGACATGATGTTGTTCTGTTCAAGTCCACACAACACATTTG 233
 Oy 1993 TAGGTGCAATGCTCTATGCTGTTGATGTTAGGATGAGAATTCACAACGAAACGCA 2052
 Db 234 TTGGCATTAATTAATTTGTCGCTGATGCTGTTCTTGAATCTACTTTGATGAAATCTAG 293
 Oy 2053 TACAGTTGGCCATGCAAGTCTAATACAGATGCAATCACTGACTTGAAGTGAAGAG 2112
 Db 294 TACAGTTGATCCCGTGAATCTGACGAGATGTAATCAACATGAGAGCTTGGAGAAGA 353
 Oy 2113 ACAATACTATTCGATCTAATGGAAGTGTAACTCACTTACGGGATACGTCGGAGTCT 2172
 Db 354 ACGGAACCATTCATTAAGGCAAGTGTGGCCACAACGCAACAGTCCAGGAAGCT 413
 Oy 2173 ATGTGATGATCTATGATGCAATACTGCTGCAACTGATGACACCCGCTGCGCAATATG 2232
 Db 414 ATGTATTTATCTCTGATCGCAACAGTGAAGGCTTAAGGCCACATTTGGAATAACAA 473
 Oy 2233 ATTAATGAACCATCTAATAATCCAGATCTAGTCTAGTTTACGACGCACTAGGAAACA 2292
 Db 474 AGGATGGCTCATCTTAACCCCTCTGCTCACTGATTGACCTCAAGTCCGGAAGAAA 533
 Oy 2293 GTGGTACCACTTACGGTGAACCAACATTTA 2326
 Db 534 GTGGCTCCCTACTCACTTGAACCAATGTTT 567

RESULT 13
 LOCUS CA929999 659 bp mRNA linear EST 30-DEC-2002
 DEFINITION MT02CA.P5.G01 Aspen apex cDNA library Populus tremuloides cDNA,
 mRNA sequence.
 ACCESSION CA929999
 VERSION CA929999
 KEYWORDS GI:27418480

SOURCE
ORGANISM Populus tremuloides (quaking aspen)
Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 659)
REFERENCE Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai
AUTHORS C.-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished
COMMENT Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
FEATURES
source 1..659
/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA library"
/note="Organ: apex"
BASE COUNT 188 a 144 c 139 g 188 t
ORIGIN
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Best Local Similarity 58.1%; Pred. No. 1.3e-30;
Matches 294; Conservative 0; Mismatches 195; Indels 17; Gaps 2;
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OY 2296 GTACCACTTACGGTGCAAAACCAATTATGCCGTTAGTCAAGTTGGCTTCTACTA 2355
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OY 2356 ATATATACCACTTTTTCACACATTTGGGCTATATGCTGTGCTTGAAGCAA 2415
DB 127 GTGTTTCAAAACCATCACCAGAGTCATTTGCGGCTTGGGACTACTGCTTGAATTTA 186
OY 2416 ATATGACAAGTATGATAGAGACTGTAGCACTGAAAGGCTGAAACAACAGTGGCTC 2475
DB 187 ACAAAGAGTCCCAAGTATAGCAAGTGGTGAAGAACAAGCTGAACAAATATGAAATT 246
OY 2476 TTTATGACAGATGTTCAATACCTCTCAGCAAAACCGAGATTAATTTGCTTACAGTATT 2535
DB 247 TTTACGC--ATGGTTTCATAGAGGTTGGTGCMAACAGATTGTCCTTAACCTACCGATG 304
OY 2536 CTAATATACGGGAAACAGTTGTTAAGATCCTCTCTTGAGCCCTGCATCCTCGCCAC 2595
DB 305 GAAATATCAAAAGAGAGCTTGGTCGTCGTTGTCCTTGAAGCCCTGTCATCTTAACCAAC 364
OY 2596 GATGAGTGT-----CAAGATGATGAAACATTTTAAATTTGTATAGTG 2640
DB 365 GTTGACGTTTGGGAGACAGCCACGGAAGCTTATTTCCCATTTTGAACGTAATATG 424
OY 2641 GATTGCTTTAGATGTGAGCGATCGATCCGAGCTTAAACAATCATTTCTTACCTC 2700
DB 425 CTTTGCTTTGATGTGAGCTATTCATCTTAACCTTTTCAAAATTAATTTATTTGGGATT 484
OY 2701 TCCATGTGACCAACCAAAATATGG 2726
DB 485 TCAACGAGAGACTTAACAGTATGG 510

RESULT 14
CA930552/c 692 bp mRNA linear EST 30-DEC-2002
LOCUS CA930552 P23.H10 Aspen apex cDNA Library Populus tremuloides cDNA,
DEFINITION MTUACA.P23.H10 Aspen apex cDNA Library Populus tremuloides cDNA,

ACCESSION mRNA sequence.
CA930552
VERSION CA930552.1 GI:27419032
KEYWORDS EST.
SOURCE Populus tremuloides (quaking aspen)
ORGANISM Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
1 (bases 1 to 692)
REFERENCE Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and Tsai
AUTHORS C.-J.
TITLE Expressed sequence tags from Aspen
JOURNAL Unpublished
COMMENT Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2915
Fax: 906 487 2915
Email: chtsai@mtu.edu.
Location/Qualifiers
FEATURES
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/organism="Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA library"
/note="Organ: apex"
BASE COUNT 199 a 147 c 153 g 193 t
ORIGIN
Query Match 5.0%; Score 140; DB 14; Length 692;
Best Local Similarity 58.1%; Pred. No. 1.4e-30;
Matches 294; Conservative 0; Mismatches 195; Indels 17; Gaps 2;
OY 2236 ATGGAACCATGATTAATCCAGATCTAGTCTAGTTTTCAGACGACATCAGGGAACAGTG 2295
DB 688 ATGGCTCATCTTAACCCCTCCTCGTCACTAGTTTTCAGCTCAAGTCGGGAAAAAGTG 629
OY 2296 GTACCACTTACGGTGCAAAACCAATTATGCCGTTAGTCAAGTTGGCTTCTACTA 2355
DB 628 GCTCCCTCCTACCTTGGAACCAATGTTATGCTTGCGCCAGGTTGGAATTTACCA 569
OY 2356 ATATATACCACTTTTTCACACATTTGGGCTATATGCTGTGCTTGAAGCAA 2415
DB 568 GTGTTTCAAAACCATCACCAGAGTCATTTGCGGCTTGGGACTACTGCTTGAATTTA 509
OY 2416 ATATGACAAGTATGATAGAGACTGTAGCACTGAAAGGCTGAAACAACAGTGGCTC 2475
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DB 448 TTTACGC--ATGGTTTCATAGAGGTTGGTGCMAACAGATTGTCCTTAACCTACCGATG 391
OY 2536 CTAATATACGGGAAACAGTTGTTAAGATCCTCTCTTGAGCCCTGCATCCTCGCCAC 2595
DB 390 GAAATATCAAAAGAGAGCTTGGTCGTCGTTGTCCTTGAAGCCCTGTCATCTTAACCAAC 331
OY 2596 GATGAGTGT-----CAAGATGATGAAACATTTTAAATTTGTATAGTG 2640
DB 330 GTTGACGTTTGGGAGACAGCCACGGAAGCTTATTTCCCATTTTGAACGTAATATG 271
OY 2641 GATTGCTTTAGATGTGAGCGATCGATCCGAGCTTAAACAATCATTTCTTACCTC 2700
DB 270 CTTTGCTTTGATGTGAGCTATTCATCTTAACCTTTTCAAAATTAATTTATTTGGGATT 211
OY 2701 TCCATGTGACCAACCAAAATATGG 2726
DB 210 TCAACGAGAGACTTAACAGTATGG 185

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RESULT 15
BU827371          588 bp  mRNA  linear  EST 15-OCT-2002
LOCUS             BU827371
DEFINITION        UK131TH03 Populus apical shoot cDNA library Populus tremula x
ACCESSION         BU827371
VERSION           BU827371.1  GI:24001037
KEYWORDS          EST.
SOURCE            Populus tremula x Populus tremuloides
ORGANISM          Populus tremula x Populus tremuloides
                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
                  ; eurosids I; Malpighiales; Salicaceae; Populus.
                  1 (bases 1 to 588)
REFERENCE         Uneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
AUTHORS           The poplar tree transcriptome: Analysis of expressed sequence tags
TITLE             from multiple libraries
JOURNAL           Unpublished
COMMENT           Contact: BHALERAO RUPALI R.
                  Umea Plant Science Center
                  Department of Plant Physiology
                  University of Umea, 901 87 Umea, Sweden
                  Tel: +46 90 786 5279
                  Fax: +46 90 786 6676
                  Email: rupali.bhalerao@plantphys.umu.se.
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                  /tissue_type="apical shoot"
                  /clone_lib="Populus apical shoot cDNA library"
BASE COUNT       176 a 128 c 130 g 154 t
ORIGIN
Query Match      4.8%; Score 133.6; DB 13; Length 588;
Best Local Similarity 60.4%; Pred. No. 1.1e-26;
Matches 220; Conservative 0; Mismatches 144; Indels 0; Gaps 0;
QY 1933 GCTGAGTACTGAGATTGCTGATGTTTGTATGATCTGAGCCCATAGTGGCTATCG 1992
DB 209 GCCCTGCTGTCGAAGAAATGACGATGTTGTTCTGCTCAAGTCCACACACACATGG 268
QY 1993 TAGTCGAATGCTCTATGTTGATGTTAGGATGGAAGATTCCACACGGAACGCA 2052
DB 269 TTGCGATTAATTAATTTGCGCTGACGCTTCTTGAACTCTACTTGTGATGAAACTTAG 328
QY 2053 TACAGTTGCGCATGCAAGCTAATACAGATGCAATCAGCTCTGACCTTGAAGAG 2112
DB 329 TACAGTTGACCCGCTGAATCTAAGGAGATGTAATCAACAATGAGCTTGGAGAGA 388
QY 2113 ACAATACTATTGATCTAATGAGAAAGTGTTAACCTTAACGAGTACAGTCCGGAGTCT 2172
DB 389 ACGGAAACCATTCATCTTAAGGCAAGTGTGGCCACAAAGGCAACAAGTCCAGGAAGCT 448
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DB 449 ATGTATTATCTGACTGCAACAAGGTGAAGGCTAGCGCCACAATTGGAAAAATACAA 508
QY 2233 ATATGGAACGATCAATAATCCAGATCTAGTCTAGTTTATAGCAGCGCATCAGGGAACA 2292
DB 509 AGGATGGCTCATCTTAACCCCTCCTGTCACCTAGTTTGACTCAAGTCAAGGAAAA 568
QY 2293 GTGG 2296
DB 569 GTGG 572

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